

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

(A) NAME: INFECTIO DIAGNOSTIC (I.D.I.) INC.
(B) STREET: 2050, BOULEVARD RENE LEVESQUE OUEST, 4E ETAGE
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(A) NAME: PICARD, FRANCOIS J.
(B) STREET: 1245, RUE DE LA SAPINIERE
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(A) NAME: OUELLETTE, MARC
(B) STREET: 1035 DE PLOERMEL
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(D) STATE: QUEBEC
(E) COUNTRY: CANADA
(F) POSTAL CODE (ZIP): G1S 3S1

(A) NAME: ROY, PAUL H.
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(C) CITY: LORETTEVILLE
(D) STATE: QUEBEC
(E) COUNTRY: CANADA
(F) POSTAL CODE (ZIP): G2A 3S1

(ii) TITLE OF INVENTION: SPECIES-SPECIFIC, GENIUS-SPECIFIC AND
UNIVERSAL DNA PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY
DETECT AND IDENTIFY COMMON BACTERIAL AND FUNGAL PATHOGENS
AND ASSOCIATED ANTIBIOTIC RESISTANCE GENES ...

(iii) NUMBER OF SEQUENCES: 174

(iv) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(vi) PRIOR APPLICATION DATA:

00989643 112004

(2) INFORMATION FOR SEQ ID NO: 1:

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Enterococcus faecium*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

TGCTTTAGCA ACAGCCTATC AG

22

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Enterococcus faecium*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

TAAACTTCTT CCGGCACTTC G

21

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Listeria monocytogenes*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

TGCGGCTATA AATGAAGAGG C

21

(2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Listeria monocytogenes*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

ATCCGATGAT GCTATGGCTT T

21

(2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Neisseria meningitidis*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

CCAGCGGTAT TGTTTGGTGG T

21

(2) INFORMATION FOR SEQ ID NO: 6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Neisseria meningitidis*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

CAGGCGGCCT TTAATAATTT C

21

(2) INFORMATION FOR SEQ ID NO: 7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Staphylococcus saprophyticus*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

AGATCGAATT CCACATGAAG GTTATTATGA

30

(2) INFORMATION FOR SEQ ID NO: 8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Staphylococcus saprophyticus*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

TCGCTTCTCC CTCAACAATC AAACATCCT

30

(2) INFORMATION FOR SEQ ID NO: 9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus agalactiae*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

TTTCACCAGC TGTATTAGAA GTA

23

(2) INFORMATION FOR SEQ ID NO: 10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus agalactiae*

009964312001

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

GTTCCCTGAA CATTATCTTT GAT

23

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida albicans*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

CAAGAAGGTT GGTACAACC CAAAGA

26

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida albicans*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

AGGTCTTACC AGTAACTTTA CCGGAT

26

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

TACTGACAAA CCATTCATGA TG

22

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs

100211 14968650

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

AACTTCGTCA CCAACGCGAA C

21

(2) INFORMATION FOR SEQ ID NO: 15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

CTGGCGCGGT ATGGTCGGTT

20

(2) INFORMATION FOR SEQ ID NO: 16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

GCCGACGTTG GAAGTGGTAA AG

22

(2) INFORMATION FOR SEQ ID NO: 17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

CCGTGTTGAA CGTGGTCAAA TCAA

25

(2) INFORMATION FOR SEQ ID NO: 18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs

(ii) MOLECULE TYPE: DNA (genomic)

TRTGTGGTGT RATWGWCCA GGAGC

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

ACAACGTGGW CAAGTWTTAG CWGCT

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

ACCATTTCWG TACCTTCTGG TAAGT

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

```
(A) NAME/KEY: misc_feature
(B) LOCATION:12
(D) OTHER INFORMATION:/note= "n = inosine"
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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

GAAATTGCAG GNAAATTGAT TGA

23

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:12
- (D) OTHER INFORMATION:/note= "n = inosine"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

TTACGCATGG CNTGACTCAT CAT

23

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:3
- (D) OTHER INFORMATION:/note= "n = inosine"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:6
- (D) OTHER INFORMATION:/note= "n = inosine"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:9
- (D) OTHER INFORMATION:/note= "n = inosine"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:12
- (D) OTHER INFORMATION:/note= "n = inosine"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:15
- (D) OTHER INFORMATION:/note= "n = inosine"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

009944 64958560

ACNKKNACNG GNGTNGARAT GTT

23

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:6
- (D) OTHER INFORMATION:/note= "n = inosine"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:9
- (D) OTHER INFORMATION:/note= "n = inosine"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:12
- (D) OTHER INFORMATION:/note= "n = inosine"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:18
- (D) OTHER INFORMATION:/note= "n = inosine"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

AYRTTNTCNC CNGGCATNAC CAT

23

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

TCGCTTCTCC

10

(2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 600 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

099896412004

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus faecium*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

TTCTTAGAGA CATTGAATAT GCCTTATGTC GGCGCAGGCG TATTGACCAG TGCATGTGCC 60
ATGGATAAAA TCATGACCAA GTATATTTTA CAAGCTGCTG GTGTGCCGCA AGTTCCTTAT 120
GTACCACTAC TTAAGAATCA ATGGAAAGAA AATCCTAAAA AAGTATTTGA TCAATGTGAA 180
GGTTCTTTGC TTTATCCGAT GTTTGTCAA CCTGCGAATA TGGGTTCTAG TGTCGGCATT 240
ACAAAGGCAG AAAACCGAGA AGAGCTGCAA AATGCTTTAG CAACAGCCTA TCAGTATGAT 300
TCTCGAGCAA TCGTTGAACA AGGAATTGAA GCGCGCGAAA TCGAAGTTGC TGTATTAGGA 360
AATGAAGATG TTCGGACGAC TTTCCTGGC GAAGTCGTAA AAGACGTAGC ATTCTATGAT 420
TATGAAGCCA AATATATCAA TAATAAAATC GAAATGCAGA TTCCAGCCGA AGTGCCGGAA 480
GAAGTTTATC AAAAAGCGCA AGAGTACGCG AAGTTAGCTT ACACGATGTT AGGTGGAAGC 540
GGATTGAGCC GGTGCGATTT CTTTTTGACA AATAAAAATG AATTATTCCT GAATGAATTA 600

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1920 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Listeria monocytogenes*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

GTGGGATTAA ACAGATTTAT GCGTGCGATG ATGGTGGTTT TCATTACTGC CAATTGCATT 60
ACGATTAACC CCGACATAAT ATTTGCAGCG ACAGATAGCG AAGATTCTAG TCTAAACACA 120
GATGAATGGG AAGAAGAAAA AACAGAAGAG CAACCAAGCG AGGTAAATAC GGGACCAAGA 180
TACGAACTG CACGTGAAGT AAGTTCACGT GATATTAAAG AACTAGAAAA ATCGAATAAA 240
GTGAGAAATA CGAACAAAGC AGACCTAATA GCAATGTTGA AAGAAAAAGC AGAAAAAGGT 300
CCAAATATCA ATAATAACAA CAGTGAACAA ACTGAGAATG CGGCTATAAA TGAAGAGGCT 360

TCAGGAGCCG ACCGACCAGC TATACAAGTG GAGCGTCGTC ATCCAGGATT GCCATCGGAT 420
 AGCGCAGCGG AAATTAAAAA AAGAAGGAAA GCCATAGCAT CATCGGATAG TGAGCTTGAA 480
 AGCCTTACTT ATCCGGATAA ACCAACAAAA GTAAATAAGA AAAAAGTGGC GAAAGAGTCA 540
 GTTGCGGATG CTTCTGAAAG TGACTTAGAT TCTAGCATGC AGTCAGCAGA TGAGTCTTCA 600
 CCACAACCTT TAAAAGCAAA CCAACAACCA TTTTCCCTA AAGTATTTAA AAAAATAAAA 660
 GATGCGGGGA AATGGGTACG TGATAAAATC GACGAAAATC CTGAAGTAAA GAAAGCGATT 720
 GTTGATAAAA GTGCAGGGTT AATTGACCAA TTATTAACCA AAAAGAAAAG TGAAGAGGTA 780
 AATGCTTCGG ACTTCCCGCC ACCACCTACG GATGAAGAGT TAAGACTTGC TTTGCCAGAG 840
 ACACCAATGC TTCTTGTTTT TAATGCTCCT GCTACATCAG AACCGAGCTC ATTCGAATTT 900
 CCACCACCAC CTACGGATGA AGAGTTAAGA CTTGCTTTGC CAGAGACGCC AATGCTTCTT 960
 GGTTTTAATG CTCTTGCTAC ATCGGAACCG AGCTCGTTCG AATTTCCACC GCCTCCAACA 1020
 GAAGATGAAC TAGAAATCAT CCGGGAAACA GCATCCTCGC TAGATTCTAG TTTTACAAGA 1080
 GGGGATTTAG CTAGTTTGAG AAATGCTATT AATCGCCATA GTCAAAATTT CTCTGATTTT 1140
 CCACCAATCC CAACAGAAGA AGAGTTGAAC GGGAGAGGCG GTAGACCAAC ATCTGAAGAA 1200
 TTTAGTTCGC TGAATAGTGG TGATTTTACA GATGACGAAA ACAGCGAGAC AACAGAAGAA 1260
 GAAATTGATC GCCTAGCTGA TTTAAGAGAT AGAGGAACAG GAAAACACTC AAGAAATGCG 1320
 GGTTTTTTAC CATTAAATCC GTTTGCTAGC AGCCCGGTTT CTTCGTTAAG TCCAAGGTA 1380
 TCGAAAATAA GCGACCGGGC TCTGATAAGT GACATAACTA AAAAAACGCC ATTTAAGAAT 1440
 CCATCACAGC CATTAAATGT GTTTAATAAA AAACTACAA CGAAAACAGT GACTAAAAAA 1500
 CCAACCCCTG TAAAGACCGC ACCAAAGCTA GCAGAACTTC CTGCCACAAA ACCACAAGAA 1560
 ACCGTACTTA GGGAAAATAA AACACCCTTT ATAGAAAAAC AAGCAGAAAC AAACAAGCAG 1620
 TCAATTAATA TGCCGAGCCT ACCAGTAATC CAAAAAGAAG CTACAGAGAG CGATAAAGAG 1680
 GAAATGAAAC CACAAACCGA GGAAAAAATG GTAGAGGAAA GCGAATCAGC TAATAACGCA 1740
 AACGGAAAAA ATCGTTCTGC TGGCATTGAA GAAGGAAAAC TAATTGCTAA AAGTGCAGAA 1800
 GACGAAAAAG CGAAGGAAGA ACCAGGGAAC CATACGACGT TAATTCCTGC AATGTTAGCT 1860
 ATTGGCGTGT TCTCTTTAGG GCGGTTTATC AAAATTATTC AATTAAGAAA AAATAATTAA 1920

(2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 415 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Neisseria meningitidis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

TACCGGTACG CTAAATATTG GTGATGTATT GGATATTATG ATTTGGGAAG CGCCGCCAGC 60
GGTATTGTTT GGTGGTGGCC TTTCTTCGAT GGGCTCGGGT AGTGCGCAAC AAACCAAGTT 120
GCCGGAGCAA CTGGTGACGG CACGTGGTAC GGTTCCTGTG CCGTTTGTTG GCGATATTTC 180
GGTGGTCGGT AAAACGCCTG GTCAGGTTCA GGAAATTATT AAAGGCCGCC TGAAAAAAT 240
GGCCAATCAG CCGCAAGTGA TGGTGCCTT GGTGCAGAAT AATGCGGCAA ATGTATCGGT 300
GATTCGCGCA GGCAATAGTG TCGGTATGCC GTTGACGGCA GCCGGTGAGC GTGTGTTGGA 360
TGCGGTGGCT GCGGTAGGTG GTTCAACGGC AAATGTGCAG GATACGAATG TGCAG 415

(2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 438 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus saprophyticus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

TCGCTTCTCC AGAAGAAATT TTAGAAACAT ATCTAGAAAA TCCCAAATTA GATAAACCGT 60
TTATATTATG TGAATACGCA CATGCAATGG GAAATTCACC AGGAGATCTT AATGCATATC 120
AAACATTAAT TGAAAAATAT GATAGTTTTA TTGGCGGTTT TGTTTGGGAA TGGTGTGATC 180
ATAGCATTCA GGTTGGGATA AAGGAAGGTA AACCAATTTT TAGATATGGT GGAGATTTTG 240
GTGAGGCCTT ACATGACGGT AATTTTTGTG TTGATGGTAT TGTTTCGCCA GATCGAATTC 300
CACATGAAGG TTATTATGAG TTAAACATG AACATAGACC TTTGAGATTG GTTAACGAAG 360
AGGATTATCG GTTTACATTG AAGAATCAAT TTGATTTTAC AAATGCGGAG GATAGTTTGA 420
TTGTTGAGGG AGAAGCGA 438

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 768 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus agalactiae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

ATGAACGTTA CACATATGAT GTATCTATCT GGAAGTCTAG TGGCTGGTGC ATTGTTATTT 60
TCACCAGCTG TATTAGAAAGT ACATGCTGAT CAAGTGACAA CTCCACAAGT GGTAAATCAT 120
GTAAATAGTA ATAATCAAGC CCAGCAAATG GCTCAAAGC TTGATCAAGA TAGCATTTCAG 180
TTGAGAAATA TCAAAGATAA TGTTCAAGGA ACAGATTATG AAAAACCGGT TAATGAGGCT 240
ATTACTAGCG TGGAAAAATT AAAGACTTCA TTGCGTGCCA ACCCTGAGAC AGTTTATGAT 300
TTGAATTCTA TTGGTAGTCG TGTAGAAGCC TTAACAGATG TGATTGAAGC AATCACTTTT 360
TCAACTCAAC ATTTAACAAA TAAGGTTAGT CAAGCAAATA TTGATATGGG ATTTGGGATA 420
ACTAAGCTAG TTATTCGCAT TTTAGATCCA TTTGCTTCAG TTGATTCAAT TAAAGCTCAA 480
GTTAACGATG TAAAGGCATT AGAACAAAAA GTTTTAACTT ATCCTGATTT AAAACCAACT 540
GATAGAGCTA CCATCTATAC AAAATCAAAA CTTGATAAGG AAATCTGGAA TACACGCTTT 600
ACTAGAGATA AAAAAGTACT TAACGTCAAA GAATTTAAAG TTTACAATAC TTAAATAAAA 660
GCAATCACAC ATGCTGTTGG AGTTCAGTTG AATCCAAATG TTACGGTACA ACAAGTTGAT 720
CAAGAGATTG TAACATTACA AGCAGCACTT CAAACAGCAT TAAATATA 768

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 421 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria meningitidis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

0988643 4958660

ATGAAAGTAG GTTTCGTCGG CTGGCGCGGT ATGGTCGGTT CGGTTTTGAT GCAGCGTATG 60
AAAGAAGAAA ACGACTTCGC CCACATTCCC GAAGCGTTTT TCTTTACCAC TTCCAACGTC 120
GGCGGCGCAC GCCCTGATTT CGGTCAGGCG GCTAAAACAT TATTGGACGC GAACAACGTT 180
GCCGAGCTGG CAAAAATGGA CATCATCGTT ACCTGCCAAG GCGGCGACTA CACCAAATCC 240
GTCTTCCAAG CCCTGCGCGA CAGCGGCTGG AACGGCTACT GGATTGACGC GGCATCCTCG 300
CTGCGTATGA AAGACGACGC GATTATCGTC CTCGACCCCG TCAACCGCAA CGTCATCGAC 360
AACGGCCTCA AAAACGGCGT GAAAACTAC ATCGGCGGCA ACTGTACCGT TTCCCTGATG 420
C 421

(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus gordonii*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

TTCATAGACG CTGAGCACGC TTTGGATCCA TCTTACGCGG CTGCTCTAGG TGTAATATT 60
GATGAGCTGT TGCTATCTCA ACCAGATTCT GGTGAGCAAG GTTTAGAAAT TGCAGGAAAA 120
TTGATTGACT CTGGGGCAGT TGATTTAGTT GTCATCGACT CTGTTGCAGC TCTTGTACCA 180
CGTGCGGAAA TCGATGGAGA TATCGGTGAT AGC 213

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 692 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus mutans*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

GGGCCGGAAT CTTCTGGTAA GACAACTGTC GCTCTTCATG CTGCTGCTCA GGCGCAAAAA 60

0909543 43004
T002T 436660

GATGGCGGTA TTGCCGCTTT CATTGATGCA GAACATGCCC TTGATCCAGC CTATGCTGCT 120
 GCTCTTGGCG TTAATATTGA TGAGCTTTTG CTTTCACAAC CAGATTCAGG AGAACAGGGT 180
 CTTGAAATTG CAGGGAAATT GATTGATTCT GGCGCTGTTG ATTTAGTTGT TGTTGACTCA 240
 GTGGCAGCTT TAGTACCACG TGCGGAGATT GACGGAGATA TTGGTAATAG TCATGTTGGC 300
 TTACAAGCAC GCATGATGAG TCAAGCGATG CGTAAATTAT CAGCTTCAAT CAATAAAACA 360
 AAAACCATTG CTATTTTTAT TAATCAATTG CGGGAAAAAG TTGGTATTAT GTTTGGTAAT 420
 CCAGAAACAA CCCCTGGCGG GCGTGCCTTG AAGTTTTATT CTTCTGTGCG TCTTGATGTC 480
 CGCGGCAATA CTCAAATTAA AGGAACCGGG GAACAAAAAG ACAGCAATAT TGGTAAAGAG 540
 ACCAAAATTA AAGTTGTTAA AAATAAAGTT GCTCCACCAT TTAAGGAAGC TTTTGTAGAA 600
 ATTATATATG GTGAAGGCAT TTCTCGTACA GGTGAATTAG TTAAGATTGC CAGTGATTG 660
 GGAATTATCC AAAAAGCTGG AGCTTGGTAC TC 692

(2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1204 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

ATGGCGAAAA AACCAAAAAA ATTAGAAGAA ATTTCAAAAA AATTGGGGC AGAACGTGAA 60
 AAGGCCTTGA ATGACGCTCT TAAATTGATT GAGAAAGACT TTGGTAAAGG ATCAATCATG 120
 CGTTTGGGTG AACGTGCGGA GCAAAGGTG CAAGTGATGA GCTCAGGTTC TTTAGCTCTT 180
 GACATTGCCC TTGGCTCAGG TGTTATCCT AAGGGACGTA TCATCGAAAT CTATGGCCCA 240
 GAGTCATCTG GTAAGACAAC GGTTGCCCTT CATGCAGTTG CACAAGCGCA AAAAGAAGGT 300
 GGGATTGCTG CCTTTATCGA TGCGGAACAT GCCCTTGATC CAGCTTATGC TGCGGCCCTT 360
 GGTGTCAATA TTGACGAATT GCTCTTGTCT CAACCAGACT CAGGAGAGCA AGGTCTTGAG 420
 ATTGCGGGAA AATTGATTGA CTCAGGTGCA GTTGATCTTG TCGTAGTCGA CTCAGTTGCT 480
 GCCCTTGTTT CTCGTGCGGA AATTGATGGA GATATCGGAG ATAGCCATGT TGGTTTGCAG 540
 GCTCGTATGA TGAGCCAGGC CATGCGTAAA CTTGGCGCCT CTATCAATAA AACCAAAACA 600

0908643 112001

ATTGCCATTT TTATCAACCA ATTGCGTGAA AAAGTTGGAG TGATGTTTGG AAATCCAGAA	660
ACAACACCGG GCGGACGTGC TTTGAAATTC TATGCTTCAG TCCGCTTGGA TGTTTCGTGGT	720
AATACACAAA TTAAGGGAAC TGGTGATCAA AAAGAAACCA ATGTCGGTAA AGAAACTAAG	780
ATTAAGGTTG TAAAAAATAA GGTAGCTCCA CCGTTTAAAG AAGCCGTAGT TGAAATTATG	840
TACGGAGAAG GAATTTCTAA GACTGGTGAG CTTTTGAAGA TTGCAAGCGA TTTGGATATT	900
ATCAAAAAAG CAGGGGCTTG GTATTCTTAC AAAGATGAAA AAATTGGGCA AGGTTCTGAG	960
AATGCTAAGA AATACTTGGC AGAGCACCCA GAAATCTTTG ATGAAATTGA TAAGCAAGTC	1020
CGTTCTAAAT TTGGCTTGAT TGATGGAGAA GAAGTTTCAG AACAAGATAC TGAAAACAAA	1080
AAAGATGAGC CAAAGAAAGA AGAAGCAGTG AATGAAGAAG TTCCGCTTGA CTTAGGCGAT	1140
GAACTTGAAA TCGAAATTGA AGAATAAGCT GTTAAAGCAG TGGAGAAATC CGCTACTTTT	1200
TCGA	1204

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 981 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pyogenes*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

ATGCGTTCAG GAAGTCTAGC TCTTGATATT GCTTGGATAG CTGGTGGTTA TCCTAAAGGA	60
CGTATCATCG AAATCTATGG TCCAGAGTCT TCCGGTAAAA CGACTGTGGC TTTACATGCT	120
GTAGCACAAG CTCAAAAAGA AGGTGGAATC GCAGCCTTTA TCGATGCCGA GCATGCGCTT	180
GATCCAGCTT ATGCTGCTGC GCTTGGGGTT AATATTGATG AACTTCTCTT GTCTCAACCA	240
GATTCTGGAG AACAAAGACT TGAAATTGCA GGTAAATTGA TTGATTCTGG TCGGTTGAC	300
CTGGTTGTTG TCGATTCACT AGCAGCTTTA GTGCCACGTG CTGAAATTGA TGGTGATATT	360
GGCGATAGCC ATGTCGGATT GCAAGCACGT ATGATGAGTC AGGCCATGCG TAAATTATCA	420
GCTTCTATTA ATAAAACAAA AACTATCGCA ATCTTTATCA ACCAATTGCG TGAAAAAGTT	480
GGTGTGATGT TTGGAAATCC TGAAACAACA CCAGGTGGTC GAGCTTTGAA ATTCTATGCT	540
TCTGTTCCGC TGGATGTGCG TGGAAACAAC CAAATTAAAG GAACTGGTGA CCAAAGATA	600

GCCAGCATTG GTAAGGAGAC CAAAATCAAG GTTGTAAAA ACAAGGTCGC TCCGCCATTT	660
AAGGTAGCAG AAGTTGAAAT CATGTATGGG GAAGGTATTT CTCGTACAGG GGAGCTTGTG	720
AAAATTGCTT CTGATTTGGA CATTATCCAA AAAGCAGGTG CTTGGTTCTC TTATAATGGT	780
GAGAAGATTG GCCAAGGTTT TGAAAATGCT AAGCGTTATT TGGCCGATCA TCCACAATTG	840
TTTGATGAAA TCGACCGTAA AGTACGTGTT AAATTTGGTT TGCTTGAAGA AAGCGAAGAA	900
GAATCTGCTA TGGCAGTAGC ATCAGAAGAA ACCGATGATC TTGCTTTAGA TTTAGATAAT	960
GGTATTGAAA TTGAAGATTA A	981

(2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus salivarius*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

GCGTATGCAC GAGCTCTAGG TGTTAATATC GATGAGCTTC TTTTGTGCGA GCCTGATTCT	60
GGTGAGCAAG GTCTCGAAAT TGCAGGTAAG CTGATTGACT CTGGTGCACT GGATTTAGTT	120
GTTGTTGACT CAGTTGCGGC CTTTCGTACCA CGTGCAGAAA TTGATGGAGA TAGTGGTGAC	180
AGTCATGTAG GACTTCAAGC GCGTATGATG AGTCAAGCCA TGCGTAAACT TTCTGCATCT	240
ATTAATAAAA CAAAACGAT TGCTATCTTT ATTAACCACT TGCCTGAAAA AGTTGGTATC	300
ATGTTTGGTGTA AC	312

(2) INFORMATION FOR SEQ ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

CTATGTGGCG CGGTATTATC	20
-----------------------	----

(2) INFORMATION FOR SEQ ID NO: 38:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

20

(2) INFORMATION FOR SEQ ID NO: 42:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

20

(2) INFORMATION FOR SEQ ID NO: 46:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

TTGAATTTGG CTTCTTCGGT

20

(2) INFORMATION FOR SEQ ID NO: 47:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

GGGATACAGA AACGGGACAT

20

(2) INFORMATION FOR SEQ ID NO: 48:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

TAAATCTTTT TCAGGCAGCG

20

(2) INFORMATION FOR SEQ ID NO: 49:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

GATGGTTTGA AGGGTTTATT ATAAG

25

(2) INFORMATION FOR SEQ ID NO: 50:

009964 4304
496860

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

20

(2) INFORMATION FOR SEQ ID NO: 54:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

CAGCTGTTAC AACGGACTGG

20

(2) INFORMATION FOR SEQ ID NO: 55:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

TCTATGATCT CGCAGTCTCC

20

(2) INFORMATION FOR SEQ ID NO: 56:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

ATCGTCACCG TAATCTGCTT

20

(2) INFORMATION FOR SEQ ID NO: 57:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

CATTCTCGAT TGCTTTGCTA

20

(2) INFORMATION FOR SEQ ID NO: 58:

099894 1000
T0027 1498660

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

CCGAAATGCT TCTCAAGATA

20

(2) INFORMATION FOR SEQ ID NO: 59:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

CTGGATTATG GCTACGGAGT

20

(2) INFORMATION FOR SEQ ID NO: 60:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

AGCAGTGTGA TGGTATCCAG

20

(2) INFORMATION FOR SEQ ID NO: 61:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

GACTCTTGAT GAAGTGCTGG

20

(2) INFORMATION FOR SEQ ID NO: 62:

039044-1300
T0027-490000

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

CTGGTCTATT CCTCGCACTC

20

(2) INFORMATION FOR SEQ ID NO: 63:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

TATGAGAAGG CAGGATTCGT

20

(2) INFORMATION FOR SEQ ID NO: 64:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

GCTTTCTCTC GAAGGCTTGT

20

(2) INFORMATION FOR SEQ ID NO: 65:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

GAGTTGCTGT TCAATGATCC

20

(2) INFORMATION FOR SEQ ID NO: 66:

09080647 12001

(2) INFORMATION FOR SEQ ID NO: 70:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

TGCTGTCATA TTGTCTTGCC

20

(2) INFORMATION FOR SEQ ID NO: 71:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

ATTATCTTCG GCGGTTGCTC

20

(2) INFORMATION FOR SEQ ID NO: 72:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

GACTATCGGC TTCCCATTCC

20

(2) INFORMATION FOR SEQ ID NO: 73:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

CGATAGAAGC AGCAGGACAA

20

(2) INFORMATION FOR SEQ ID NO: 74:

09989643 4 2004

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

CTGATGGATG CGGAAGATAC

20

(2) INFORMATION FOR SEQ ID NO: 75:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

GCCTTATGTA TGAACAAATG G

21

(2) INFORMATION FOR SEQ ID NO: 76:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

GTGACTTTWG TGATCCCTTT TGA

23

(2) INFORMATION FOR SEQ ID NO: 77:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

TCCAATCATT GCACAAAATC

20

(2) INFORMATION FOR SEQ ID NO: 78:

09089643-12001

(2) INFORMATION FOR SEQ ID NO: 82:

(2) INFORMATION FOR SEQ ID NO: 86:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

CCTTTACTCC AATAATTTGG CT

22

(2) INFORMATION FOR SEQ ID NO: 87:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

TTTCATCTAT TCAGGATGGG

20

(2) INFORMATION FOR SEQ ID NO: 88:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

GGAGCAACAT TCTTTGTGAC

20

(2) INFORMATION FOR SEQ ID NO: 89:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

TGTGCCTGAA GAAGGTATTG

20

(2) INFORMATION FOR SEQ ID NO: 90:

0999543-1000
"000000" 0499560

(ii) MOLECULE TYPE: DNA (genomic)

CGTGTTACTT CACCACCACT

20

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

TATCTTATCG TTGAGAAGGG ATT

23

(2) INFORMATION FOR SEQ ID NO: 92:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

CTACACTTGG CTTAGGATGA AA

22

(2) INFORMATION FOR SEQ ID NO: 93:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

CTATCTGATT GTTGAAGAAG GATT

24

(2) INFORMATION FOR SEQ ID NO: 94:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

24

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

22

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

22

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

27

(2) INFORMATION FOR SEQ ID NO: 98:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98:

ATTGCTGTGA ATATTTTTTG AGTTGAA

27

(2) INFORMATION FOR SEQ ID NO: 99:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

GTGATCGAAA TCCAGATCC

19

(2) INFORMATION FOR SEQ ID NO: 100:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:

ATCCTCGGTT TTCTGGAAG

19

(2) INFORMATION FOR SEQ ID NO: 101:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

CTGGTCATAC ATGTGATGG

19

(2) INFORMATION FOR SEQ ID NO: 102:

00221 E4358560

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102:

GATGTTACCC GAGAGCTTG

19

(2) INFORMATION FOR SEQ ID NO: 103:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

TTAAGCGTGC ATAATAAGCC

20

(2) INFORMATION FOR SEQ ID NO: 104:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:

TTGCGATTAC TTCGCCAACT

20

(2) INFORMATION FOR SEQ ID NO: 105:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

TTTACTAAGC TTGCCCCCTTC

20

(2) INFORMATION FOR SEQ ID NO: 106:

7002716495650

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:

AAAAGGCAGC AATTATGAGC

20

(2) INFORMATION FOR SEQ ID NO: 107:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION:9
 - (D) OTHER INFORMATION:/note= "n = inosine"
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION:12
 - (D) OTHER INFORMATION:/note= "n = inosine"
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION:15
 - (D) OTHER INFORMATION:/note= "n = inosine"
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION:18
 - (D) OTHER INFORMATION:/note= "n = inosine"
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION:21
 - (D) OTHER INFORMATION:/note= "n = inosine"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

AAAYATGATNA CNGGNGCNGC NCARATGGA

29

(2) INFORMATION FOR SEQ ID NO: 108:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid

```
(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
  (A) NAME/KEY: misc_feature
  (B) LOCATION:3
  (D) OTHER INFORMATION:/note= "n = inosine"

(ix) FEATURE:
  (A) NAME/KEY: misc_feature
  (B) LOCATION:6
  (D) OTHER INFORMATION:/note= "n = inosine"

(ix) FEATURE:
  (A) NAME/KEY: misc_feature
  (B) LOCATION:9
  (D) OTHER INFORMATION:/note= "n = inosine"

(ix) FEATURE:
  (A) NAME/KEY: misc_feature
  (B) LOCATION:12
  (D) OTHER INFORMATION:/note= "n = inosine"
```

CCNACNGTNC KNCCRCCYTC RCG

23

(2) INFORMATION FOR SEQ ID NO: 109:

```
(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 29 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
    (A) NAME/KEY: misc_feature
    (B) LOCATION:6
    (D) OTHER INFORMATION:/note= "n = inosine"

(ix) FEATURE:
    (A) NAME/KEY: misc_feature
    (B) LOCATION:12
    (D) OTHER INFORMATION:/note= "n = inosine"

(ix) FEATURE:
    (A) NAME/KEY: misc_feature
    (B) LOCATION:15
    (D) OTHER INFORMATION:/note= "n = inosine"

(ix) FEATURE:
    (A) NAME/KEY: misc feature
```

(B) LOCATION:18

(D) OTHER INFORMATION:/note= "n = inosine"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:

CARYTNATHG TNGCNGTNAA YAARATGGA

29

(2) INFORMATION FOR SEQ ID NO: 110:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 831 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:

ATGAAAAACA CAATACATAT CAACTTCGCT ATTTTTTTTAA TAATTGCAAA TATTATCTAC 60
AGCAGCGCCA GTGCATCAAC AGATATCTCT ACTGTTGCAT CTCCATTATT TGAAGGAACT 120
GAAGGTTGTT TTTTACTTTA CGATGCATCC ACAAACGCTG AAATTGCTCA ATTCAATAAA 180
GCAAAGTGTG CAACGCAAAT GGCACCAGAT TCAACTTTCA AGATCGCATT ATCACTTATG 240
GCATTTGATG CGGAAATAAT AGATCAGAAA ACCATATTCA AATGGGATAA AACCCCCAAA 300
GGAATGGAGA TCTGGAACAG CAATCATACA CCAAAGACGT GGATGCAATT TTCTGTTGTT 360
TGGGTTTCGC AAGAAATAAC CCAAAAAATT AGATTAAATA AAATCAAGAA TTATCTCAAA 420
GATTTTGATT ATGGAAATCA AGACTTCTCT GGAGATAAAG AAAGAAACAA CGGATTAACA 480
GAAGCATGGC TCGAAAGTAG CTTAAAAATT TCACCAGAAG AACAAATTCA ATTCCTGCGT 540
AAAATTATTA ATCACAATCT CCCAGTTAAA AACTCAGCCA TAGAAAACAC CATAGAGAAC 600
ATGTATCTAC AAGATCTGGA TAATAGTACA AAAGTGTATG GGAAACTGG TGCAGGATTC 660
ACAGCAAATA GAACCTTACA AAACGGATGG TTTGAAGGGT TTATTATAAG CAAATCAGGA 720
CATAAATATG TTTTGTGTC CGCACTTACA GGAACTTGG GGTCGAATTT AACATCAAGC 780
ATAAAAGCCA AGAAAAATGC GATCACCATT CTAAACACAC TAAATTTATA A 831

(2) INFORMATION FOR SEQ ID NO: 111:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 846 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

20021124090650

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

TTGAAAAAGT TAATATTTTT AATTGTAATT GCTTTAGTTT TAAGTGCATG TAATTCAAAC	60
AGTTCACATG CCAAAGAGTT AAATGATTTA GAAAAAAAT ATAATGCTCA TATTGGTGT	120
TATGCTTTAG ATACTAAAAG TGGTAAGGAA GTAAAATTTA ATTCAGATAA GAGATTTGCC	180
TATGCTTCAA CTTCAAAGC GATAAATAGT GCTATTTTGT TAGAACAAGT ACCTTATAAT	240
AAGTTAAATA AAAAAGTACA TATTAACAAA GATGATATAG TTGCTTATTC TCCTATTTTA	300
GAAAAATATG TAGGAAAAGA TATCACTTTA AAAGCACTTA TTGAGGCTTC AATGACATAT	360
AGTGATAATA CAGCAAACAA TAAATTATA AAAGAAATCG GTGGAATCAA AAAAGTTAAA	420
CAACGTCTAA AAGAACTAGG AGATAAGTA ACAAATCCAG TTAGATATGA GATAGAATTA	480
AATTACTATT CACCAAAGAG CAAAAAGAT ACTTCAACAC CTGCTGCTTT CGGTAAGACT	540
TTAAATAAAC TTATCGCAA TGGAAAATTA AGCAAAGAAA AAAAAAATT CTTACTTGAT	600
TTAATGTAA ATAATAAAG CGGAGATACT TTAATTAAAG ACGGTGTTCC AAAAGACTAT	660
AAGGTTGCTG ATAAAAGTGG TCAAGCAATA ACATATGCTT CTAGAAATGA TGTGCTTTT	720
GTTTATCCTA AGGGCCAATC TGAACCTATT GTTTTAGTCA TTTTACGAA TAAAGACAAT	780
AAAAGTGATA AGCCAAATGA TAAGTTGATA AGTGAAACCG CCAAGAGTGT AATGAAGGAA	840
TTTTAA	846

(2) INFORMATION FOR SEQ ID NO: 112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 555 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

ATGTCCGCGA GCACCCCCC CATAACTCTT CGCCTCATGA CCGAGCGCGA CCTGCCGATG	60
CTCCATGACT GGCTCAACCG GCCGCACATC GTTGAGTGGT GGGGTGGCGA CGAAGAGCGA	120
CCGACTCTTG ATGAAGTGCT GGAACACTAC CTGCCCAGAG CGATGGCGGA AGAGTCCGTA	180
ACACCGTACA TCGCAATGCT GGGCGAGGAA CCGATCGGCT ATGCTCAGTC GTACGTCGCG	240
CTCGGAAGCG GTGATGGCTG GTGGGAAGAT GAACTGATC CAGGAGTGCG AGGAATAGAC	300
CAGTCTCTGG CTGACCCGAC ACAGTTGAAC AAAGGCCTAG GAACAAGGCT TGTCCGCGCT	360

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

ATGAACAAAA ATATAAAATA TTCTCAAAC TTTTAAACGA GTGAAAAAGT ACTCAACCAA	60
ATAATAAAAC AATTGAATTT AAAAGAAACC GATACCGTTT ACGAAATTGG AACAGGTAAA	120
GGGCATTTAA CGACGAAACT GGCTAAAATA AGTAAACAGG TAACGTCTAT TGAATTAGAC	180
AGTCATCTAT TCAACTTATC GTCAGAAAAA TTAAATCGA ATACTCGTGT CACTTTAATT	240
CACCAAGATA TTCTACAGTT TCAATTCCCT AACAAACAGA GGTATAAAAT TGTTGGGAAT	300
ATTCCCTTACC ATTTAAGCAC ACAAATTATT AAAAAAGTGG TTTTGAAG CCATGCGTCT	360
GACATCTATC TGATTGTTGA AGAAGGATTC TACAAGCGTA CCTTGATAT TCACCGAACA	420
CTAGGGTTGC TCTTGCACAC TCAAGTCTCG ATTCAGCAAT TGCTTAAGCT GCCAGCGGAA	480
TGCTTTCATC CTAAACCAAG AGTAAACAGT GTCTTAATAA AACTTACCCG CCATACCACA	540
GATGTTCCAG ATAAATATTG GAAGCTATAT ACGTACTTTG TTTCAAATG GGTCAATCGA	600
GAATATCGTC AACTGTTTAC TAAAAATCAG TTTCATCAAG CAATGAAACA CGCCAAAGTA	660
AACAATTTAA GTACCGTTAC TTATGAGCAA GTATTGTCTA TTTTAAATAG TTATCTATTA	720
TTTAACGGGA GGAAATAA	738

(2) INFORMATION FOR SEQ ID NO: 115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 735 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

ATGAACGAGA AAAATATAAA ACACAGTCAA AACTTTATTA CTTCAAACA TAATATAGAT	60
AAAATAATGA CAAATATAAG ATTAAATGAA CATGATAATA TCTTTGAAAT CGGCTCAGGA	120
AAAGGGCATT TTACCCTTGA ATTAGTACAG AGGTGTAATT TCGTAACTGC CATTGAAATA	180
GACCATAAAT TATGCAAAAC TACAGAAAAT AACTTGTTG ATCACGATAA TTTCCAAGTT	240
TTAAACAAGG ATATATTGCA GTTTAAATTT CCTAAAAACC AATCCTATAA AATATTTGGT	300
AATATACCTT ATAACATAAG TACGGATATA ATACGCAAAA TTGTTTTTGA TAGTATAGCT	360
GATGAGATTT ATTTAATCGT GGAATACGGG TTTGCTAAAA GATTATTAAA TACAAAACGC	420
TCATTGGCAT TATTTTAAAT GGCAGAAGTT GATATTTCTA TATTAAGTAT GGTTCCAAGA	480

0999643-112001

(2) INFORMATION FOR SEO ID NO: 116:

(A) LENGTH: 1029 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116:

ATGAATAAAA	TAAAAGTCGC	AATTATCTTC	GGCGGTTGCT	CGGAGGAACA	TGATGTGTCTG	60
GTAAAATCCG	CAATAGAAAT	TGCTGCGAAC	ATTAATACTG	AAAAATTCGA	TCCGCACTAC	120
ATCGGAATTA	CAAAAAACGG	CGTATGGAAG	CTATGCAAGA	AGCCATGTAC	GGAATGGGAA	180
GCCGATAGTC	TCCCCGCCAT	ATTCTCCCCG	GATAGGAAAA	CGCATGGTCT	GCTTGTCTATG	240
AAAGAAAGAG	AATACGAAAC	TCGGCGTATT	GACGTGGCTT	TCCCGGTTTT	GCATGGCAAA	300
TGCGGGGAGG	ATGGTGCGAT	ACAGGGTCTG	TTTGAATTGT	CTGGTATCCC	CTATGTAGGC	360
TGCGATATTC	AAAGCTCCGC	AGCTTGCAATG	GACAAATCAC	TGGCCTACAT	TCTTACAAAA	420
AATGCGGGCA	TCGCCGTCCC	CGAATTTCAA	ATGATTGAAA	AAGGTGACAA	ACCGGAGGCG	480
AGGACGCTTA	CCTACCCTGT	CTTTGTGAAG	CCGGCACGGT	CAGGTTCTGTC	CTTTGGCGTA	540
ACCAAAGTAA	ACAGTACGGA	AGAACTAAAC	GCTGCGATAG	AAGCAGCAGG	ACAATATGAT	600
GGAAAAATCT	TAATTGAGCA	AGCGATTTCG	GGCTGTGAGG	TCGGCTGCGC	GGTCATGGGA	660
AACGAGGATG	ATTTGATTGT	CGGCGAAGTG	GATCAAATCC	GGTTGAGCCA	CGGTATCTTC	720
CGCATCCATC	AGGAAAACGA	GCCGGAAAAA	GGCTCAGAGA	ATGCGATGAT	TATCGTTCCA	780
GCAGACATTC	CGGTCGAGGA	ACGAAATCGG	GTGCAAGAAA	CGGCAAAGAA	AGTATATCGG	840
GTGCTTGGAT	GCAGAGGGCT	TGCTCGTGTT	GATCTTTTTT	TGCAGGAGGA	TGGCGGCATC	900
GTTCTAAACG	AGGTCAATAC	CCTGCCCCGT	TTTACATCGT	ACAGCCGCTA	TCCACGCATG	960
GCGGCTGCCG	CAGGAATCAC	GCTTCCCCGA	CTAATTGACA	GCCTGATTAC	ATTGGCGATA	1020

GAGAGGTGA

1029

(2) INFORMATION FOR SEQ ID NO: 117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1031 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

ATGAAAAAAAA TTGCCGTTTT ATTTGGAGGG AATTCTCCAG AATACTCAGT GTCACTAACC	60
TCAGCAGCAA GTGTGATCCA AGCTATTGAC CCGCTGAAAT ATGAAGTAAT GACCATTGGC	120
ATCGCACCAA CAATGGATTG GTATTGGTAT CAAGGAAACC TCGCGAATGT TCGCAATGAT	180
ACTTGGCTAG AAGATCACAA AAAGTGTAC CAGCTGACTT TTTCTAGCCA AGGATTTATA	240
TTAGGAGAAA AACGAATCGT CCCTGATGTC CTCTTTCCAG TCTTGCATGG GAAGTATGGC	300
GAGGATGGCT GTATCCAAGG ACTGCTTGAA CTAATGAACC TGCCTTATGT TGGTTGCCAT	360
GTCGCTGCCT CCGCATTATG TATGAACAAA TGGCTCTTGC ATCAACTTGC TGATACCATG	420
GGAATCGCTA GTGCTCCAC TTTGCTTTTA TCCCGCTATG AAAACGATCC TGCCACAATC	480
GATCGTTTTA TTCAAGACCA TGGATTCCCG ATCTTTATCA AGCCGAATGA AGCCGGTTCT	540
TCAAAAGGGA TCACAAAAGT AACTGACAAA ACAGCGCTCC AATCTGCATT AACGACTGCT	600
TTTGCTTACG GTTCTACTGT GTTGATCCAA AAGGCGATAG CGGGTATTGA AATTGGCTGC	660
GGCATCTTAG GAAATGAGCA ATTGACGATT GGTGCTTGTG ATGCGATTTC TCTTGTCGAC	720
GGTTTTTTTG ATTTTGAAGA GAAATACCAA TTAATCAGCG CCACGATCAC TGTCCCAGCA	780
CCATTGCCTC TCGCGCTTGA ATCACAGATC AAGGAGCAGG CACAGCTGCT TTATCGAAAC	840
TTGGGATTGA CGGGTCTGGC TCGAATCGAT TTTTTCGTCA CCAATCAAGG AGCGATTAT	900
TTAAACGAAA TCAACACCAT GCCGGGATTT ACTGGGCACT CCCGCTACCC AGCTATGATG	960
GCGGAAGTCG GGTTATCCTA CGAAATATTA GTAGAGCAAT TGATTGCACT GGCAGAGGAG	1020
GACAAACGAT G	1031

(2) INFORMATION FOR SEQ ID NO: 118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 809 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Abiotrophia adiacens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118:

TGGTGCTATC TTAGTAGTAT CTGCAGCTGA TGGTCCAATG CCTCAAACAC GTGAACACAT	60
CTTATTATCA CGTCAAGTAG GTGTTCCCTTA CATCGTTGTA TTCTTAAACA AAGTTGACAT	120
GGTTGACGAT GAAGAATTAT TAGAATTAGT AGAAATGGAA GTTCGTGACT TATTATCAGA	180
ATACGATTTT CCAGGCGATG ACACTCCAGT TGTTGCAGGT TCTGCTTTAC GCGCTTTAGA	240
AGGCGACGCT TCATACRAAG AAAAAATCTT AGAATTAATG GCTGCTGTTG ACGAATACAT	300
TCCAACCTCA GAACGYGACG TTGACAAACC ATTCATGATG CCAGTTGAAG ACGTGTTCCTC	360
AATCACAGGT CGTGGTACTG TTGCTACAGG TCGTGTGAA CGTGGACAAG TTCGTGTTGG	420
TGACGAAGTT GAAATCGTTG GTATTTTCTA AGAACTTCA AAAACAACCTG TAACTGGTGT	480
TGAAATGTTC CGTAAATTGT TAGACTACGC TGAAGCAGGG GATAACATTG GTACATTATT	540
ACGTGGTGTT ACACGTGACA ACATCGAAGT TGGACAAGTT CTTGCTAAAC CAGGAACAAT	600
CACTCCACAT ACTAAATTCA AAGCTGAAGT TTACGTATTA ACTAAAGAAG AAGGTGGACG	660
TCATACTCCA TTCTTCTCTA ACTACCGTCC TCAATTCTAC TTCCGTACAA CAGACATCAC	720
TGGTGTTTGT GTGTTACCAG AAGGCGTTGA AATGGTAATG CCTGGTGATA ACGTAACTAT	780
GGAAGTTGAA TTAATTCACC CAGTAGCGA	809

(2) INFORMATION FOR SEQ ID NO: 119:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 817 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Abiotrophia defectiva*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

CGGCGCGATC CTCGTTGTAT CTGCTGCTGA CGGCCCAATG CCACAACTC GTGAACACAT	60
CCTCTTGTCT CGTCAAGTTG GTGTTCCCTTA CATCGTAGTA TTCTTGAACA AAGTTGACAT	120

(2) INFORMATION FOR SEQ ID NO: 120:

(A) LENGTH: 754 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:

CTCTGTCAAA	TGGGACAAAA	ACAGATTTGA	AGAAATCATC	AAGGAAACCT	CCAACTTCGT	60
CAAGAAGGTT	GGTTACAACC	CAAAGACTGT	TCCATTTCGT	CCAATCTCTG	GTTGGAATGG	120
TGACAACWTG	ATTGAASCAT	CCACCAACTG	TCCATGGTAC	AAGGGTTGGG	AAAAGGAAAC	180
CAAATCCGGT	AAAGTTACTG	GTAAGACCTT	GTTAGAAGCT	ATTGACGCTA	TTGAACCACC	240
AACCAGACCA	ACCGACAAAC	CATTGAGATT	GCCATTTRCA	GATGTTTACA	AGATCGGTGG	300
TATTGGTACT	GTGCCAGTCG	GTAGAGTTGA	AACTGGTATC	ATCAAAGCCG	GTATGGTWGT	360
TACTTTTCGCC	CCAGCTGGTG	TTACCACTGA	AGTCAARTCC	GTTGAAATGC	ATCACGAACA	420
ATTGGCTGAA	GGTGTTCCAG	GTGACAATGT	TRGTTTCAAC	GTTAAGAACR	TTTCCGTTAA	480
AGAAATTAGA	AGAGGTAACG	TTTGTGGTGA	CTCCAAGAAC	GATCCACCAA	AGGGTTGTGA	540

CTCTTTCAAT GCCCAAGTCA TTGTTTTGAA CCATCCAGGT CAAATCTCTG CTGGTTACTC	600
TCCAGTCTTG GATTGTCACR CTGCCCACAT TGCTTGTAAG TTCGACRCTT TGGTTGAAAA	660
GATTGACAGA AGAACTGGTA AGRAATTGGA AGAAAATCCA AAATTCGTCA AATCCGGTGA	720
TGCTGCTATC GTCAAGATGG TCCCAACCAA ACCA	754

(2) INFORMATION FOR SEQ ID NO: 121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 753 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida glabrata*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:

TCTGTCAAGT GGGATGAATC CAGATTCGCT GAAATCGTTA AGGAAACCTC CAACTTCATC	60
AAGAAGGTCG GTTACAACCC AAAGACTGTT CCATTCGTCC CAATCTCTGG TTGGAACGGT	120
GACAACATGA TTGAAGCCAC CACCAACGCT TCCTGGTACA AGGGTTGGGA AAAGGAAACC	180
AAGGCTGGTG TCGTCAAGGG TAAGACCTTG TTGGAAGCCA TTGACGCTAT CGAACCACCA	240
ACCAGACCAA CTGACAAGCC ATTGAGATTG CCATTGCAAG ATGTCTACAA GATCGGTGGT	300
ATCGGTACGG TGCCAGTCGG TAGAGTCGAA ACCGGTGTCA TCAAGCCAGG TATGGTTGTT	360
ACCTTCGCCC CAGCTGGTGT TACCACTGAA GTCAAGTCCG TTGAAATGCA CCACGAACAA	420
TTGACTGAAG GTTTGCCAGG TGACAACGTT GGTTCACAG TTAAGAACGT TTCCGTTAAG	480
GAAATCAGAA GAGGTAATGT CTGTGGTGAC TCCAAGAAGC ACCCACCAA GGCTGCTGCT	540
TCTTTCACG CTACCGTCAT TGTCTTGAAC CACCCAGGTC AAATCTCTGC TGGTTACTCT	600
CCAGTTTTGG ACTGTACAC CGCCACATT GCTTGTAAGT TCGAAGAATT GTTGAAAAAG	660
AACGACAGAA GATCCGGTAA GAAGTTGGAA GACTCTCCAA AGTTCTTGAA GTCCGGTGAC	720
GCTGCTTTGG TTAAGTTCGT TCCATCCAAG CCA	753

(2) INFORMATION FOR SEQ ID NO: 122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 752 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

F00271 2496660

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida krusei*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

CCGTTAAGTG GGATGAAAAC AGATTTGAAG AAATTGTCAA GGAAACCCAA AACTTCATCA 60
AGAAGGTTGG TTACAACCCA AAGACTGTTT CATTCGTTCC AATCTCTGGT TGAATGGTG 120
ACAACATGAT TGAAGCATCC ACCAACTGTC CATGGTACAA GGGTTGGACT AAGGAAACCA 180
AGGCAGGTGT TGTTAAGGGT AAGACCTTAT TAGAAGCAAT CGATGCTATT GAACCACCTG 240
TCAGACCAAC CGAAAAGCCA TTAAGATTAC CATTACAAGA TGTTTACAAG ATTGGTGGTA 300
TTGGTACTGT GCCAGTCGGT AGAGTCGAAA CCGGTGTCAT TAAGCCAGGT ATGGTTGTCA 360
CTTTTGCTCC AGCAGGTGTC ACCACCGAAG TCAAATCCGT TGAAATGCAC CATGAACAAT 420
TAGAACAAGG TGTTCCAGGT GATAACGTTG GTTTCAACGT TAAGAACGTY TCTGTCAAGG 480
ATATCAAGAG AGGTAACGTT TGTGGTGA CTCAAGAACGA CCCACCAATG GGTGCAGCTT 540
CTTTCAATGC TCAAGTCATT GTCTTGAACC ACCCTGGTCA AATTTCCGCT GGTTACTCTC 600
CAGTCTTGA TTGTCACACT GCCCACATTG CATGTAAGTT CGACGAATTA ATCGAAAAGA 660
TTGACAGAAG AACTGGTAAG TCTGTTGAAG ACCATCCAAA GTCYGTCAAG TCTGGTGATG 720
CAGCTATCGT CAAGATGGTC CCAACCAAGC CA 752

(2) INFORMATION FOR SEQ ID NO: 123:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 754 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida parapsilosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

CTCAGTCAAA TGGGACAAGA RCAGATACGA AGAAATTGTC AAGGAACTT CCAACTTCGT 60
CAAGAAGGTT GGTTACAACC CTAAAGCTGT CCCATTCGTC CCAATCTCTG GTTGGAAACGG 120
TGACAATATG ATTGAACCAT CAACCAACTG TCCATGGTAC AAGGGTTGGG AAAAGGAAAC 180
TAAAGCTGGT AAGGTTACCG GTAAGACCTT GTTGGAAAGCT ATCGATGCTA TCGARCCACC 240

(2) INFORMATION FOR SEQ ID NO: 124:

(A) LENGTH: 753 base pairs

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida tropicalis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124:

TCTGTAAAT	GGGACAARAA	CAGATTTGAA	GAAATTATCA	AGGAAACYTC	TAACTTCGTC	60
AAGAAGGTTG	GTTACAACCC	TAAGGCTGTT	CCATTCGTTT	CAATCTCWGG	TTGGAATGGT	120
GACAACATGA	TTGAAGCTTC	TACCAACTGT	CCATGGTACA	AGGGTTGGGA	AAAAGAAACC	180
AAGGCTGGTA	AGGTTACCGG	TAAGACTTTG	TTGGAAGCCA	TTGATGCTAT	TGAACCACCT	240
TCAAGACCAA	CTGACAAGCC	ATTGAGATTG	CCATTGCAAG	ATGTTTACAA	GATTGGTGGT	300
ATTGGTACTG	TGCCAGTCGG	TAGAGTTGAA	ACTGGTGTCA	TCAAAGCCGG	TATGGTTGTT	360
ACTTTYGCCC	CAGCTGGTGT	TACCACTGAA	GTCAAATCCG	TYGAAATGCA	CCACGAACAA	420
TTGGCTGAAG	GTGTCCCAGG	TGACAATGTT	GGTTTCAACG	TTAAGAACGT	TTCTGTAAAA	480
GAAATTAGAA	GAGGTAACGT	TTGTGGTGAC	TCCAAGAACG	ATCCACCAAA	GGGTTGTGAC	540
TCTTTCAACG	CTCAAGTTAT	TGTCTTGAAC	CACCCAGGTC	AAATYTCTGC	TGGTTACTCT	600
CCAGTCTTGG	ATTGTCACAC	TGCTCATATT	GCTTGTAAT	TCGACACCTT	GGTTGAAAAG	660
ATTGACAGAA	GAAGTGGTAA	GAAATTGGAA	GAAATCCAA	AATTCGTCAA	ATCCGGGTGAT	720

GCTGCTATTG TCAAGATGGT TCCAACCAAA CCA

753

(2) INFORMATION FOR SEQ ID NO: 125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 814 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium accolens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

CGGCGCTATC CTGGTTGTTG CTGCAACCGA TGGCCCGATG CCGCAGACCC GCGAGCACGT	60
TCTGCTTGCT CGCCAGGTTG GCGTTCCTTA CATCCTCGTT GCACTGAACA AGTGCGACAT	120
GGTTGATGAT GAGGAAATCA TCGAGCTCGT GGAGATGGAG ATCTCCGAGC TGCTCGCAGA	180
GCAGGACTAC GATGAGGAAG CTCCTATCGT TCACATCTCC GCTCTGAAGG CACTCGAGGG	240
TGACGAGAAG TGGGTACAGT CCATCGTTGA CCTGATGGAT GCCTGCGACA ACTCCATCCC	300
TGATCCGGAG CGCGCTACCG ATCAGCCGTT CTTGATGCCT ATCGAGGACA TCTTCACCAT	360
TACCGGCCGC GGTACCGTTG TTACCGGCCG TGTGAGCGT GGTCGTCTGA ACGTCAACGA	420
GGACGTTGAG ATCATCGGTA TCCAGGAGAA GTCCCAGAAC ACCACCGTTA CCGGTATCGA	480
GATGTTCCGC AAGATGATGG ACTACACCGA GGCTGGCGAC AACTGTGGTC TGCTTCTGCG	540
TGGTACCAAG CGTGAGGACG TTGAGCGTGG CCAGGTTGTT ATCAAGCCGG GCGCTTACAC	600
CCCTCACACC AAGTTCGAGG GTTCCGTCTA CGTCCTGAAG AAGGAAGAGG GCGGCCGCCA	660
CACCCCGYTC ATGAACAACT ACCGTCCTCA GTTCTACTTC CGCACCACCG ACGTTACCGG	720
TGTTGTGAAC CTGCCTGAGG GCACCGAGAT GGTTATGCCT GGCGACAACG TTGAGATGTC	780
TGTTGAGCTC ATCCAGCCTG TTGCTATGGA CGAG	814

(2) INFORMATION FOR SEQ ID NO: 126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 814 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

09989643-112001

(A) ORGANISM: *Corynebacterium diphtheriae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126:

CGGCGCAATC CTCGTTGTTG CTGCCACCGA CGGCCCAATG CCTCAGACCC GTGAGCACGT	60
TCTGCTCGCT CGCCAGGTCG GCGTTCCTTA CATCCTCGTT GCTCTGAACA AGTGCGACAT	120
GGTTGATGAT GAGGAAATCA TCGAGCTCGT CGAGATGGAG ATCCRTGAGC TGCTCGCTGA	180
GCAGGATTAC GACGAAGAGG CTCCAATCAT CCACATCTCC GCACTGAAGG CTCTTGAGGG	240
CGACGAGAAG TGGACCCAGT CCATCATCGA CCTCATGCAG GCTTGCKATG ATTCCATCCC	300
AGACCCAGAG CGTGAGACCG ACAAGCCATT CCTCATGCCT ATCGAGGACA TCTTCACCAT	360
CACCGGCCGC GGTACCGTTG TTACCGGCCG TGTTGAGCGT GGCTCCCTGA AGGTCAACGA	420
GGACGTCGAG ATCATCGGTA TCCGCGAGAA KGCTACCACC ACCACCGTTA CCGGTATCGA	480
GATGTTCCGT AAGCTTCTCG ACTACACCGA GGCTGGCGAC AACTGTGGTC TGCTTCTCCG	540
TGGCGTTAAG CGCGAAGACG TTGAGCGTGG CCAGGTTGTT GTTAAGCCAG GCGCTTACAC	600
CCCTCACACC GAGTTCGAGG GCTCTGTCTA CGTTCTGTCC AAGGACGAGG GTGGCCGCCA	660
CACCCCATTC TTCGACAACT ACCGCCACA GTTCTACTTC CGCACCACCG ACGTTACCGG	720
TGTTGTGAAG CTTCTGAGG GCACCGAGAT GGTCATGCCT GGCGACAACG TCGACATGTC	780
CGTCACCCTG ATCCAGCCTG TCGCTATGGA TGAG	814

(2) INFORMATION FOR SEQ ID NO: 127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 814 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium genitalium*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127:

CGGCGCCATC CTGGTTGTTG CTGCAACCGA TGGCCCGATG CCGCAGACCC GTGAGCACGT	60
TCTGCTGGCT CGCCAGGTTG GCGTTCGTA CATCCTAGTT GCACTGAACA AGTGCGACAT	120
GGTTGATGAT GAGGAGCTGC TGGAGCTCGT CGAGATGGAG GTCCGCGAGC TGCTGGCTGA	180
GCAGGACTTC GACGAGGAAG CACCTGTTGT TCACATCTCC GCACTGAAGG CCCTGGAGGG	240
CGACGAGAAG TGGGCTAAGC AGATCCTGGA GCTCATGGAG GCTTGCGACA ACTCCATCCC	300

GGATCCGGAG CGCGAGACCG ACAAGCCGTT CCTGATGCCG GTTGRGGACA TCTTCACCAT	360
TACCGGCCGC GGTACCGTTG TTACCGGCCG TGTTGAGCGT GGCCTCCTGA ACCTGAACGA	420
CGAGGTCGAG ATCCTGGGCA TCCGCGAGAA GTCCACCAAG ACCACCGTTA CCTCCATCGA	480
GATGTTCAAC AAGCTGCTGG ACACCGCAGA GGCTGGCGAC AACGCCGCAC TGCTGCTGCG	540
TGGCCTGAAG CGCGAAGATG TTGAGCGTGG TCAGATCGTT GCTAAGCCGG GCGAGTACAC	600
CCCCCACACC GAGTTCGAGG GCTCCGTCTA CGTTCTGTCC AAGGACGAGG GTGGCCGCCA	660
CACCCCGTTC TTCGACAACT ACCGTCCGCA GTTCTATTTC CGCACCACCG ACGTTACCGG	720
TGTTGTGAAG CTGCCGGAGG GCACCGAGAT GGTATGCCG GCGACAACG TTGACATGTC	780
CGTCACCCTG ATCCAGCCGG TTGCTATGGA CGAG	814

(2) INFORMATION FOR SEQ ID NO: 128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 814 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium jeikeium*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128:

CGGCGCCATC CTGGTTGTTG CCGCAACCGA TGGCCCGATG CCGCAGACCC GCGAGCACGT	60
TCTGCTGGCY CGCCAGGTTG GCGTTCCGTA CATCCTGGTT GCACTGAACA AGTGTGACAT	120
GGTTGACGAT GAGGAGCTGC TGGAGCTCGT CGAGATGGAG GTCCGCGAGC TGCTGGCTGA	180
GCAGGACTTC GACGAGGAAG CTCCGGTTGT TCACATCTCC GCACTGAAGG CCCTGGAGGG	240
CGACGAGAAG TGGGCTAACC AGATTCTCGA GCTGATGCAG GCTTGCGACG AGTCTATCCC	300
GGATCCGGAG CGCGAGACCG ACAAGCCGTT CCTGATGCCG GTTGWGGACA TCTTCACCAT	360
TACCGGTCGC GGTACCGTTG TTACCGGCCG TGTTGAGCGT GGCATCCTGA ACCTGAACGA	420
CGAGGTTGAG ATCCTGGGTA TCCGCGAGAA GTCCAGAAG ACCACCGTTA CCTCCATCGA	480
GATGTTCAAC AAGCTGCTGG ACACCGCAGA GGCTGGCRAC AACGCTGCAC TGCTGCTGCG	540
TGGTCTGAAG CGCGAGGACG TTGAGCGTGG CCAGATCATC GCTAAGCCGG GCGAGTACAC	600
CCCCCACACC GAGTTCGAGG GCTCCGTCTA CGTTCTGTCC AAGGACGAGG GCGGCCGCCA	660
CACCCCGTTC TTCGACAACT ACCGTCCGCA GTTCTACTTC CGCACCACCG ACGTTACCGG	720

T0027-4958660

TGTTGTGAAG CTGCCTGAGG GCACCGAGAT GGTATGCCC GGCGACAACG TYGACATGTC 780
CGTCACCCTG ATCCAGCCGG TTGCTATGGA CGAG 814

(2) INFORMATION FOR SEQ ID NO: 129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 748 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium pseudodiphtheriticum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

CGGCGCTATC TTGGTTGTTG CAGCTACCGA CGGCCCAATG CCACAGACTC GCGAGCACGT 60
TCTGCTGGCT CGCCAGGTTG GCGTTCCTTA CATCCTGGTT GCACTAAACA AGTGCGACAT 120
GGTTGACGAC GAGGAAATCC TCGAGCTCGT CGAGATGGAG ATCCGCGAAT TGCTGGCTGA 180
CCAGGAATTC GACGAAGAAG CTCCAATCGT TCACATCTCC GCAGTCGGCG CCTTGAAGG 240
CGAAGAGAGG TGGGTAAACG CCATCGTTGA ACTGATGGAT GCTTGTGACG AGTCGATCCC 300
TGATCCAGAC CGTGCTACCG ACAAGCCATT CCTGATGCCT ATCGAGGACA TCTTCACCAT 360
TACCGGTCGT GGCACCGTTG TTACGGGTCTG TGTGAGCGT GGTTCCTGA AGGTCAACGA 420
AGAAGTCGAG ATCATCGGCA TCAAGGAAAA GTCCCAGAAG ACCACCATCA CCGGTATCGA 480
AATGTTCCGC AAGATGCTGG ACTACACCGA GGCCGGCGAC AACGCTGGTC TGCTGCTTCG 540
CGGTACCAAG CGTGAAGACG TTGAGCGTGG ACAGGTTATC GTTGCTCCAG GTGCTTACAG 600
CACCCACAAG AAGTTCGAAG GTTCCGTCTA CGTTCTTTCC AAGGACGAGG GCGGCCGCCA 660
CACCCCGTTC TTCGACAACT ACCGTCCTCA GTTCTACTTC CGCACCACCG ACGTTACCGG 720
TGTTGTTACC CTGCCTGAGG GCACCGAG 748

(2) INFORMATION FOR SEQ ID NO: 130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 813 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

0998543-112001

(A) ORGANISM: *Corynebacterium striatum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130:

GGCGCTATCT TGGTTGTTGC TGCAACCGAT GGCCCGRTGC CGCAGACCCG CGAGCACGTT 60
CTTCTGGCTC GCCAGGTTGG CGTTCCTTAC ATCCTCGTTG CACTGAACAA GTGCGACATG 120
GTTGACGACG AGGAAATTAT CGAGCTCGTC GAGATGGAGA TCCGCGAACT GCTCGCAGAG 180
CAGGACTACG ATGAGGAAGC TCCGATCGTT CACATCTCTG CTCTGAAGGC TCTTGAGGGC 240
GRCGAGAAGT GGGTACAGGC TATCGTTGAC CTGATGCAGG CTTGCGATGA CTCCATCCCG 300
GATCCGGAGC GCGAGCTGGA CAAGCCGTTT CTGATGCCAA TCGAGGACAT CTTACCATC 360
ACCGGCCGCG GTACCGTTGT TACTGGCCGT GTTGAGCGTG GCTCCCTGAA CGTCAACGAG 420
GACGTTGAGA TCATCGGTAT CCAGGACARG TCCATCTCCA CCACCGTTAC CGGTATCGAG 480
ATGYTCCGCA AGATGATGGA CTACACCGAG GCTGGCGACA ACTGTGGTCT GCTTCTGCGT 540
GGTACCAAGC GTGAAGAGGT TGAGCGCGGC CAGGTTGTTA TTAAGCCGGG CGCTTACACC 600
CCTCACACCC AGTTCGAGGG TTCCGTCTAC GTCCTGAAGA AGGAAGAGGG CGGCCGCCAC 660
ACCCCGTTCA TGGACAACTA CCGTCCGCAG TTCTACTTCC GCACCACCGA CGTTACCGGC 720
GTCATCAAGC TGCCTGAGGG CACCGAGATG GTTATGCCTG GCGACAACGT CGAGATGTCY 780
GTCGAGCTGA TCCAGCCGGT CGCTATGGAC GAG 813

(2) INFORMATION FOR SEQ ID NO: 131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus avium*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:

CGGAGCTATC TTAGTAGTAT CTGCTGCTGA TGGCCCTATG CCTCAAATC GTGAACACAT 60
CTTGTTATCT CGTAACGTTG GTGTTCTTA CATCGTTGTA TTCTTAAACA AAATGGATAT 120
GGTTGACGAT GAAGAATTAC TTGAATTAGT TGAAATGGAA GTTCGTGACT TATTAAGTGA 180
ATACGACTTC CCAGGCGACG AACTCCAGT TATCGCAGGT TCAGCGTTGA AAGCTTTAGA 240
AGGCGACGCT TCATACGAAG AAAAAATCTT AGAATTAATG GCTGCTGTTG ACGAATATAT 300

CCCAACACCA GTTCGTGATA CTGACAAACC ATTCATGATG CCAGTCGAAG ACGTATTCTC 360
AATCACTGGT CGTGGTACTG TTGCAACTGG TCGTGTGAA CGTGGACAAG TTCGCGTTGG 420
TGACGAAGTT GAAATCGTAG GTATCGCTGA CGAAACTGCT AAAACAACCTG TTACAGGTGT 480
TGAAATGTTC CGTAAATTGT TAGACTACGC TGAAGCAGGT GACAACATCG GTGCTTTGTT 540
ACGTGGTGTT GCACGTGAAG ATATCCAACG TGGACAAGTA TTGGCTAAAC CAGCTTCAAT 600
CACTCCACAT ACAAATTCT CTGCAGAAGT TTATGTTCTA ACTAAGAAG AAGGTGGACG 660
TCATACTCCA TTCTTCACTA ACTACCGTCC TCAGTTCTAC TTCCGTACAA CTGACGTAAC 720
TGGTGTAGTT GATCTACCAG AAGGTACTGA AATGGTWTAG CCTGGGGATA ACGTAACTAT 780
GGAAGTTGAA TTGATYCACC CAATYCGGGT AGAAGAC 817

(2) INFORMATION FOR SEQ ID NO: 132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecalis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132:

CGGAGCTATC TTAGTAGTTT CTGCTGCTGA TGGTCCTATG CCTCAAACAC GTGAACATAT 60
CTTATTATCA CGTAACGTTG GTGTACCATA CATCGTTGTA TTCTTAAACA AAATGGATAT 120
GGTTGATGAC GAAGAATTAT TAGAATTAGT AGAAATGGAA GTTCGTGACT TATTATCAGA 180
ATACGATTTC CCAGGCGATG ATGTTCCAGT TATCGCAGGT TCTGCTTTGA AAGCTTTAGA 240
AGGCGACGAG TCTTATGAAG AAAAAATCTT AGAATTAATG GCTGCAGTTG ACGAATATAT 300
CCCAACTCCA GAACGTGATA CTGACAAACC ATTCATGATG CCAGTCGAAG ACGTATTCTC 360
AATCACTGGA CGTGGTACTG TTGCTACAGG ACGTGTGAA CGTGGTGAAG TTCGCGTTGG 420
TGACGAAGTT GAAATCGTTG GTATTAAAGA CGAAACATCT AAAACAACYG TTACAGGTGT 480
TGAAATGTTC CGTAAATTAT TAGACTACGC TGAAGCAGGC GACAACMTCG GTGCTTTATT 540
ACGTGGTGTA GCACGTGAAG ATATCGAACG TGGACAAGTA TTAGCTAAAC CAGCTACAAT 600
CACTCCACAC ACAAATTCA AAGCTGAAGT ATACGTATTA TCAAGAAG AAGGCGGACG 660
TCACACTCCA TTCTTCACTA ACTACCGTCC TCAATTCTAC TTCCGTACAA CAGACGTTAC 720

09989643-112001

(2) INFORMATION FOR SEQ ID NO: 133:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133:

(2) INFORMATION FOR SEQ ID NO: 134:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 809 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus gallinarum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134:

CGGTGCGATC TTAGTAGTAT CTGCTGCTGA CGGTCCTATG CCTCAAACCTC GTGAACACAT 60
CTTGTTATCA CGTAACGTTG GCGTACCATA CATCGTTGTT TTCTTGAACA AAATGGATAT 120
GGTTGAYGAC GAAGAATTGC TAGAATTAGT TGAAATGGAA GTTCGTGACC TATTGTCTGA 180
ATATGACTTC CCAGGCGACG ATGTTCTGT AATCGCCGGT TCTGCTTTGA AAGCTCTTGA 240
AGGAGATCCT TCATACGAAG AAAAAATCAT GGAATTGATG GCTGCAGTTG ACGAATACGT 300
TCCAACCTCA GAACGTGATA CTGACAAACC ATTCATGATG CCAGTCGAAG ACGTATTCTC 360
AATCACTGGA CGTGGTACTG TTGCTACAGG CCGTGTTGAA CGTGGACAAG TTCGCGTTGG 420
TGATGAAGTA GAAATCGTTG GTATTGCTGA CGAAACTGCT AAAACAACCTG TAACAGGTGT 480
TGAAATGTTC CGTAAATTGT TAGACTATGC TGAAGCAGGG GATAACATTG GTGCATTGCT 540
ACGTGGGGTT GCTCGTGAAG ACATCCAACG TGGACAAGTA TTGGCTAAAG CTGGTACAAT 600
CACACCTCAT ACAAATTCA AAGCTGAAGT TTATGTTTTG ACAAAGAAG AAGGTGGACG 660
TCACACTCCA TTCTTCACTA ACTACCGTCC TCAGTTCTAC TTCCGTACAA CTGACGTAAC 720
TGGTGTGTT GAATTACCAG AAGGAACTGA AATGGTGATG CCTGGCGACA ACGTGACCAT 780
CGACGTTGAA TTGATRCACC CAATCGCTC 809

(2) INFORMATION FOR SEQ ID NO: 135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 823 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Gardnerella vaginalis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135:

TGGCGCAATC CTCGTGGTTG CTGCTACCGA CGGTCCAATG GCTCAGACCC GTGAACACGT 60
CTTGCTTGCT AAGCAGGTCG GCGTTCCAAA AATTCTTGTT GCTTTGAACA AGTGCGATAT 120
GGTTGACGAC GAAGAGCTTA TCGATCTCGT TGAAGAAGAG GTCCGTGACC TCCTCGAAGA 180
AAACGGCTTC GATCGCGATT GCCCAGTCYT CCGTACTTCC GCTTACGGCG CTTTGCATGA 240
TGACGCTCCA GACCACGACA AGTGGGTTAGA GACCGTCAAG GAACTCATGA AGGCTGTTGA 300

CGAGTACATC CCAACCCCAA CTCACGATCT TGACAAGCCA TTCTTGATGC CAATCGAAGA 360
 TGTGTTACAC ATCTCCGGTC GTGGTYCCGT TGTCACCGGT CGTGTGAGC GTGGTAAGCT 420
 CCCAATCAAC ACCCCAGTTG AGATCGTTGG TTTGCGCGAT ACCCAGACCA CCACCGTCAC 480
 CTCTATCGAG ACCTTCCACA AGCAGATGGA TGAGGCAGAG GCTGGCGATA AACTGGTCT 540
 TCTTCTCCGC GGTATCAACC GTACCGACGT TGAGCGTGGT CAGGTTGTGG CTGCTCCAGG 600
 TTCTGTGACT CCACACACCA AGTTCGAAGG CGAAGTTTAC GTCTTGACCA AGGACGAAGG 660
 TGGCCGTCAC TCGCCATTCT TCTCCAATA CCGTCCACAG TTCTACTTCC GTACCACCGA 720
 TGTTACTGGC GTTATCACCT TGCCAGACGG CATCGAAATG GTTCAGCCAG GCGATCACGC 780
 AACCTTCACT GTTGAGTTGA TCCAGGCTAT CGCAATGGAA GAG 823

(2) INFORMATION FOR SEQ ID NO: 136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Listeria innocua*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 136:

CGGAGCTATC TTAGTAGTAT CTGCTGCTGA TGGCCCAATG CCACAACTC GTGAACATAT 60
 CTTACTTTCA CGTCAAGTTG GTGTTCCATA CATCGTTGTA TTCATGAACA AATGTGACAT 120
 GGTGACGAT GAAGAATTAC TAGAATTAGT TGAAATGGAA ATTCGTGATC TATTAAGTGA 180
 ATATGAATTC CCTGGCGATG ACATTCCTGT AATCAAAGGT TCAGCTCTTA AAGCACTTCA 240
 AGGTGAAGCT GACTGGGAAG CTAAAATTGA CGAGTTAATG GAAGCTGTAG ATTCTTACAT 300
 TCCAACCTCA GAACGTGATA CTGACAAACC ATTCATGATG CCAGTTGAGG ATGTATTCTC 360
 AATCACTGGT CGTGGAACAG TTGCAACTGG ACGTGTGAA CGTGGACAAG TTAAAGTTGG 420
 TGACGAAGTA GAAGTTATCG GTATTGAAGA AGAAAGCAAA AAAGTAGTAG TAACTGGAGT 480
 AGAAATGTTT CGTAAATTAC TAGACTACGC TGAAGCTGGC GACAACATTG GCGCACTTCT 540
 ACGTGGTGTT GCTCGTGAAG ATATCCAACG TGGTCAAGTA TTAGCTAAAC CAGGTTGAT 600
 TACTCCACAC ACTAACTTCA AAGCTGAAAC TTATGTTTTA ACTAAAGAAG AAGGTGGACG 660
 TCACACTCCA TTCTTCAACA ACTACCGCCC ACAATTCTAT TTCCGTACTA CTGACGTAAC 720

0959643-11004

TGGTATTGTT ACACTTCCAG AAGGTACTGA AATGGTAATG CCTGGTGATA ACATTGAGCT 780
TGCAGTTGAA CTAATTGCAC CAATCGCTAT CGAAGAC 817

(2) INFORMATION FOR SEQ ID NO: 137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 818 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Listeria ivanovii*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:

CGGAGCTATC TTAGTAGTAT CTGCTGCTGA TGGTCCAATG CCACAAACTC GTGAACATAT 60
TCTTACTTTC ACGTCAAGTT GGTGTTCCAT ACATCGTTGT ATTCATGAAC AAATGTGACA 120
TGGTTGACGA TGAAGAATTA CTTGAATTAG TTGAAATGGA AATTCGTGAT CTATTAAGT 180
AATATGAATT CCCTGGCGAC GACATTCCTG TAATCAAAGG TTCAGCTCTT AAAGCACTTC 240
AAGGTGAAGC TGATTGGGAA GCTAAAATTG ACGAGTTAAT GGAAGCTGTA GATTCTTACA 300
TTCCAAGTCC AGAACGTGAT ACTGACAAAC CATTATGAT GCCAGTTGAG GATGTATTCT 360
CAATCACTGG TCGTGGAACA GTTGCAACTG GACGTGTTGA ACGTGGACAA GTTAAAGTTG 420
GTGACGAAGT AGAAGTTATC GGTATTGAAG AAGAAAGCAA AAAAGTAGTA GTAAGTGGAG 480
TAGAAATGTT CCGTAAATTA CTAGACTACG CTGAAGCTGG CGACAACATT GGCGCACTTC 540
TACGTGGTGT TGCTCGTGAA GATATCCAAC GTGGTCAAGT ATTAGCTAAA CCAGGTTCTGA 600
TTACTCCACA TACTAACTTC AAAGCTGAAA CTTATGTTTT AACTAAAGAA GAAGGTGGAC 660
GTCATACTCC ATTCTTCAAC AACTACCGCC CACAATTCTA TTTCCGTACT ACTGACGTAA 720
CTGGTATTGT TACTTCCCA GAAGGTACTG AAATGGTAAT GCCTGGTGAT AACATTGAGC 780
TTGCAGTTGA ACTAATTGCA CCAATCGCTA TCGAAGAC 818

(2) INFORMATION FOR SEQ ID NO: 138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

0998964 " 1 2001

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Listeria monocytogenes*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138:

CGGAGCTATC TTAGTAGTAT CTGCTGCTGA TGGCCCAATG CCACAAACTC GTGAACATAT 60
CTTACTTTCA CGTCAAGTTG GTGTTCCATA CATCGTTGTA TTCATGAACA AATGTGACAT 120
GGTTGACGAT GAAGAATTAC TAGAATTAGT TGAAATGGAA ATTCGTGATC TATTAAGTGA 180
ATATGAATTC CCTGGCGATG ACATTCCTGT AATCAAAGGT TCAGCTCTTA AAGCACTTCA 240
AGGTGAAGCT GACTGGGAAG CTAAAATTGA CGAGTTAATG GAAGCTGTAG ATTCTTACAT 300
TCCAACCTCCW GAACGTGATA CTGACAAACC ATTCATGATG CCAGTTGAGG ATGTATTCTC 360
AATCACTGGT CGTGGAACAG TTGCAACTGG ACGTGTTGAA CGTGGAACAAG TTAAAGTTGG 420
TGACGAAGTA GAAGTTATCG GTATCGAAGA AGAAAGCAAA AAAGTAGTAG TAACTGGAGT 480
AGAAATGTTT CGTAAATTAC TAGACTACGC TGAAGCTGGC GACAACATTG GCGCACTTCT 540
ACGTGGTGTT GCTCGTGAAG ATATCCAACR TGGTCAAGTA TTAGCTAAAC CAGGTTTCGAT 600
TACTCCACAC ACTAACTTCA AAGCTGAAAC TTATGTTTTA ACTAAAGAAG AAGGTGGACG 660
TCACACTCCA TTCTTCAACA ACTACGCCC ACAATTCTAT TTCCGTACTA CTGACGTAAC 720
TGGTATTGTT ACACTTCCAG AAGGTACTGA AATGGTAAYG CCTGGTGATA ACATTGAGCT 780
TGCAGTTGAA CTAATTGCAC CAATCGCTAT CGAAGAC 817

(2) INFORMATION FOR SEQ ID NO: 139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Listeria seeligeri*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:

CGGAGCTATC TTAGTAGTAT CTGCTGCTGA TGGCCCAATG CCACAAACTC GTGAACATAT 60
CTTACTTTCA CGTCAAGTTG GTGTTCCATA CATCGTTGTA TTCATGAACA AATGTGACAT 120
GGTTGACGAT GAAGAATTAC TTGAATTAGT TGAAATGGAA ATTCGTGATC TATTAAGTGA 180
ATATGAATTC CCTGGTGATG ACATTCCTGT AATCAAAGGT TCAGCTCTTA AAGCACTTCA 240

AGGTGAAGCT GACTGGGAAG CTAAAATTGA CGAGTTAATG GAAGCTGTAG ATTCTTACAT	300
TCCAACCTCCA GAACGTGATA CTGACAAACC ATTCATGATG CCAGTTGAGG ATGTATTCTC	360
AATCACTGGT CGTGGAACTG TTGCAACTGG ACGTGTGAA CGTGGACAAG TTAAAGTTGG	420
TGACGAAGTA GAAGTTATCG GTATTGAAGA AGAAAGCAAA AAAGTAATAG TAACTGGAGT	480
AGAAATGTTC CGTAAATTAC TAGACTACGC TGAAGCTGGC GACAACATTG GCGCACTTCT	540
ACGTGGTGTT GCTCGTGAAG ATATCCAACG TGGTCAAGTA TTAGCTAAAC CAGGTTCGAT	600
TACTCCACAT ACTAACTTCA AAGCTGAAAC TTATGTTTTA ACTAAAGAAG AAGGTGGACG	660
TCACACTCCA TTCTTCAACA ACTACCGCCC ACAATTCTAT TTCCGTACTA CTGACGTAAC	720
TGGTATTGTT ACACCTCCAG AAGGTACTGA AATGGTAATG CCTGGTGATA ACATTGAGCT	780
TGCAGTTGAA CTAATTGCAC CAATCGCTAT CGAAGAC	817

(2) INFORMATION FOR SEQ ID NO: 140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 814 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140:

CGGTGGTATC TTAGTAGTAT CTGCTGCTGA CGGTCCAATG CCACAACTC GTGAACACAT	60
TCTTTTATCA CGTAACGTTG GTGTACCAGC ATTAGTAGTA TTCTTAAACA AAGTTGACAT	120
GGTTGACGAT GAAGAATTAT TAGAATTAGT AGAAATGGAA GTTCGTGACT TATTAAGCGA	180
ATATGACTTC CCAGGTGACG ATGTACCTGT AATCGCTGGT TCAGCATTAR AAGCTTTAGA	240
AGGCGATGCT CAATACGAAG AAAAAATCTT AGAATTARTG GAAGCTGTAG ATACTTACAT	300
TCCAACCTCCA GAACGTGATT CTGACAAACC ATTCATGATG CCAGTTGAGG ACGTATTCTC	360
AATCACTGGT CGTGGTACTG TTGCTACAGG CCGTGTGAA CGTGGTCAA TCAAAGTTGG	420
TGAAGAAGTT GAAATCATCG GTTTACATGA CACATCTAAA ACAACTGTTA CAGGTGTTGA	480
AATGTTCCGT AAATTATTAG ACTACGCTGA AGCTGGTGAC AACATTGGTG CATTATTACG	540
TGGTGTTGCT CGTGAAGACG TACAACGTGG TCAAGTATTA GCTGCTCCTG GTTCAATTAC	600
ACCACATACT GAATTCAAAG CAGAAGTATA CGTATTATCA AAAGACGAAG GTGGACGTCA	660

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CACTCCATTC TTCTCAAAC ATCGTCCACA ATTCTATTTTC CGTACTACTG ACGTAACTGG 720
TGTTGTTTAC TTACCAGAAG GTACTGAAAT GGTAATGCCT GGTGATAACG TTGAAATGAC 780
AGTAGAATTA ATCGCTCCAA TCGCGATTGA AGAC 814

(2) INFORMATION FOR SEQ ID NO: 141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 814 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus epidermidis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141:

CGGCGGTATC TTAGTTGTAT CTGCTGCTGA CGGTCCAATG CCACAACTC GTGAACACAT 60
CTTATTATCA CGTAACGTTG GTGTACCAGC ATTAGTTGTA TTCTTAAACA AAGTTGACAT 120
GGTAGACGAC GAAGAATTAT TAGAATTAGT TGAAATGGAA GTTCGTGACT TATTAAGCGA 180
ATATGACTTC CCAGGTGACG ATGTACCTGT AATCGCTGGT TCTGCATTAA AAGCATTAGA 240
AGGCGATGCT GAATACGAAC AAAAAATCTT AGACTTAATG CAAGCAGTTG ATGATTACAT 300
TCCAACCTCA GAACGTGATT CTGACAAACC ATTCATGATG CCAGTTGAGG ACGTATTCTC 360
AATCACTGGT CGTGGTACTG TTGCTACAGG CCGTGTTGAA CGTGGTCAAA TCAAAGTWGG 420
TGAAGAAGTT GAAATCATCG GTATGCACGA AACTTCTAAA ACAACTGTTA CTGGTGTAGA 480
AATGTTCCGT AAATTATTAG ACTACGCTGA AGCTGGTGAC AACATCGGTG CTTTATTACG 540
TGGTGTGCA CGTGAAGACG TACAACGTGG TCAAGTATTA GCTGCTCCTG GTTCTATTAC 600
ACCACACACA AAATTCAAAG CTGAAGTATA CGTATTATCT AAAGATGAAG GTGGACGTCA 660
CACTCCATTC TTCCTAACT ATCGCCCAACA ATTCTATTTTC CRTACTACTG ACGTAACTGG 720
TGTTGTAAAC TTACCAGAAG GTACAGAAAT GGTATGCCT GGCACAAACG TTGAAATGAC 780
AGTTGAATTA ATCGCTCCAA TCGCTATCGA AGAC 814

(2) INFORMATION FOR SEQ ID NO: 142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus saprophyticus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142:

CGGAGCTATC TTAGTAGTAT CTGCTGCTGA TGGCCCAATG CCACAAACTC GTGAACACAT 60
TCTTTTATCA CGTRACGTTG GTGYTCCAGC ATTAGTTGTA TTCTTAAACA AAGTTGACAT 120
GGTTGACGAY GAAGAATTAT TAGAATTRGT AGAAATGGAA GTTCGTGRCT TATTAAGCGA 180
ATATGACTTC CCAGGTGACG ATGTACCTGT AATCTCTGGT TCTGCATTAA AAGCTTTAGA 240
AGGCGACGCT GACTATGAGC AAAAAATCTT AGACTTAATG CAAGCTGTTG ATGACTYCAT 300
TCCAACACCA GAACGTGATT CTGACAAACC ATTCATGATG CCAGTTGAGG ACGTATTCTC 360
AATCACTGGT CGTGGTACTG TTGCTACAGG CCGTGTGAA CGTGGTCAAA TCAAAGTCGG 420
TGAAGAAATC GARATCATCG GTATGCAAGA AGAATCAAGC AAAACAACTG TTACTGGTGT 480
AGAAATGTTC CGTAAATTAT TAGACTACGC TGAAGCTGGT GACAACATTG GTGCATTATT 540
ACGTGGTGTT TCACGTGATG ATGTACAACG TGGTCAAGTT TTAGCTGCTC CTGGTACTAT 600
CACACCACAT ACAAATTCA AAGCGGATGT TTACGTTTTA TCTAAAGATG AAGGTGGTCG 660
TCATACGCCA TTCTTCACTA ACTACCGCCC ACAATTCTAT TTCCGTACTA CTGACGTAAC 720
TGGTGTGTTT AACTTACCAG AAGGTACTGA AATGGTTATG CCTGGCGATA ACGTTGAAAT 780
GGATGTTGAA TTAATTTCTC CAATCGCTAT TGAAGAC 817

(2) INFORMATION FOR SEQ ID NO: 143:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 817 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus simulans*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143:

CGGCGGTATC TTAGTAGTAT CTGCTGCAGA TGGTCCAATG CCACAAACTC GTGAACACAT 60
CTTATTATCA CGTAACGTTG GTGTACCAGC TTTAGTTGTA TTCTTAAACA AAGCTGACAT 120
GGTTGACGAC GAAGAATTAT TAGAATTAGT TGAAATGGAA GTTCGTGACT TATTATCTGA 180

ATACGACTTC CCTGGTGACG ATGTACCAGT TATCGTTGGT TCTGCATTAA AAGCTTTAGA 240
 AGGCGACCCA GAATACGAAC AAAAAATCTT AGACTTAATG CAAGCTGTAG ATGACTACAT 300
 CCCAACTCCA GAACGTGACT CTGATAAACC ATTCATGATG CCAGTTGAGG ACGTATTCTC 360
 AATCACTGGT CGTGGTACTG TAGCAACAGG CCGTGTGAA CGTGGTCAA TCAAAGTCGG 420
 TGAAGAAGTT GAAATCATCG GTATCACTGA AGAAAGCAAG AAAACAACAG TTACAGGTGT 480
 AGAAATGTTC CGTAAATTAT TAGACTACGC TGAAGCTGGT GACAACATCG GTGCTTTATT 540
 ACGTGGTGTT GCACGTGAAG ACGTACAACG TGGACAAGTA TTAGCAGCTC CTGGCTCTAT 600
 TACTCCACAC ACAAATTC AAGCTGATGT TTACGTTTTA TCTAAAGAAG AAGGTGGACG 660
 TCATACTCCA TTCTTCACTA ACTACCGCCC ACAATTCTAC TTCCGTACTA CTGACGTAAC 720
 TGGCGTTGTT CACTTACCAG AAGGTACTGA AATGGTTATG CCTGGCGATA ACGTAGAAAT 780
 GACTGTTGAA TTGATCGCTC CAATCGCGAT TGAAGAC 817

(2) INFORMATION FOR SEQ ID NO: 144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus agalactiae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144:

CGGAGCTATC CTTGTAGTTG CTTCAACTGA TGGACCAATG CCACAAACTC GTGAGCACAT 60
 CCTTCTTTCA CGTCAAGTTG GTGTTAAACA CCTTATCGTA TTCATGAACA AAGTTGACCT 120
 TGTGATGAT GAAGAATTGC TTGAATTGGT TGAAATGGAA ATTCGTGACC TTCTTTCAGA 180
 ATACGACTTC CCAGGTGATG ACCTTCCAGT TATCCAAGGT TCAGCTCTTA AAGCACTTGA 240
 AGGCGACGAA AAATACGAAG ACATCATCAT GGAATTGATG AGCACTGTTG ATGAGTACAT 300
 TCCAGAACCA GAACGTGATA CTGACAAACC TTTACTTCTT CCAGTTGAAG ATGTATTCTC 360
 AATCACTGGA CGTGGTACAG TTGCTTCAGG ACGTATCGAC CGTGGTACTG TTCGTGTCAA 420
 CGACGAAGTT GAAATCGTTG GTATTAAAGA AGATATCCAA AAAGCAGTTG TTACTGGTGT 480
 TGAAATGTTC CGTAAACAAC TTGACGAAGG TCTTGCAAGG GACAACGTTG GTGTTCTTCT 540
 TCGTGGTGTT CAACGTGATG AAATCGAACG TGGTCAAGTT CTTGCTAAAC CAGGTTCAAT 600

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CAACCCACAC ACTAAATTTA AAGGTGAAGT TTACATCCTT TCTAAAGAAG AAGGTGGACG 660
TCATACTCCA TTCTTCAACA ACTACCGTCC ACAATTCTAC TTCCGTACAA CTGACGTAAC 720
AGGTTCAATC GAACTTCCAG CAGGAACAGA AATGGTTATG CCTGGTGATA ACGTTACTAT 780
CGAAGTTGAA TTGATTCACC CAATCGCCGT AGAACAA 817

(2) INFORMATION FOR SEQ ID NO: 145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145:

CGGAGCTATC CTTGTAGTAG CTTCAACTGA CGGACCAATG CCACAAACTC GTGAGCACAT 60
CCTTCTTTCA CGTCAGGTTG GTGTAAACA CCTTATCGTC TTCATGAACA AAGTTGACTT 120
GGTTGACGAC GAAGAATTGC TTGAATTGGT TGAAATGGAA ATCCGTGACC TATTGTCAGA 180
ATACGACTTC CCAGGTGACG ATCTTCCAGT TATCCAAGGT TCAGCACTTA AAGCTCTTGA 240
AGGTGACTCT AAATACGAAG ACATCGTTAT GGAATTGATG AACACAGTTG ATGAGTATAT 300
CCCAGAACCA GAACGTGACA CTGACAAACC ATTGCTTCTT CCAGTCGAGG ACGTATTCTC 360
AATCACTGGA CGTGGTACAG TTGCTTCAGG ACGTATCGAC CGTGGTATCG TTAAAGTCAA 420
CGACGAAATC GAAATCGTTG GTATCAAAGA AGAACTCRA AAAGCAGTTG TTACTGGTGT 480
TGAAATGTTC CGTAAACAAC TTGACGAAGG TCTTGCTGGA GATAACGTAG GTGTCCTTCT 540
TCGTGGTGTT CAACGTGATG AAATCGAACG TGGACAAGTT ATCGCTAAAC CAGGTTCAAT 600
CAACCCACAC ACTAAATTCA AAGGTGAAGT CTACATCCTT ACTAAAGAAG AAGGTGGACG 660
TCACACTCCA TTCTTCAACA ACTACCGTCC ACAATTCTAC TTCCGTACTA CTGACGTTAC 720
AGGTTCAATC GAACTTCCAG CAGGTACTGA AATGGTAATG CCTGGTGATA ACGTGACAAT 780
CGACGTTGAG TTGATTCACC CAATCGCCGT AGAACAA 817

(2) INFORMATION FOR SEQ ID NO: 146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 base pairs
- (B) TYPE: nucleic acid

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(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus salivarius*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146:

CGGTGCGATC CTTGTAGTAG CATCTACTGA CGGACCAATG CCACAAACTC GTGAGCACAT	60
CCTTCTTTCA CGTCAGGTTG GTGTAAACA CCTTATCGTC TTCATGAACA AAGTTGACTT	120
GGTTGACGAT GAAGAATTGC TTGAATTGGT TGAAATGGAA ATCCGTGACC TTCTTTCAGA	180
ATACGATTTC CCAGGTGATG ACATTCCAGT TATCCAAGGT TCAGCTCTTA AAGCTCTTGA	240
AGGTGATTCT AAATACGAAG ACATCATCAT GGACTTGATG AACACTGTTG ACGAATACAT	300
CCCAGAACCA GAACGTGACA CTGACAAACC ATTGTTGCTT CCAGTCGAAG ACGTATTCTC	360
AATCACTGGT CGTGGTACTG TTGCTTCAGG ACGTATCGAC CGTGGTGTTG TTCGTGTCAA	420
TGACGAAGTT GAAATCGTTG GTCTTAAAGA AGACATCCA AAAGCAGTTG TTACTGGTGT	480
TGAAATGTTT CGTAAACAAC TTGACGRAGG TATTGCCGGA GATAACGTCG GTGTTCTTCT	540
TCGTGGTATC CAACGTGATG AAATCGAACG TGGTCAAGTA TTGGCTGCAC CTGGTTCAAT	600
CAACCCACAC ACTAAATTCA AAGGTGAAGT TTACATCCTT TCTAAAGAAG AAGGTGGACG	660
TCACACTCCA TTCTTCAACA ACTACCGTCC ACAGTTCTAC TTCCGTACAA CTGACGTAAC	720
AGGTTCAATC GAACTTCCTG CAGGTACTGA AATGGTTATG CCTGGTGATA ACGTGACTAT	780
CGACGTTGAG TTGATCCACC CAATCGCCGT TGAACAA	817

(2) INFORMATION FOR SEQ ID NO: 147:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 897 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Agrobacterium tumefaciens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147:

AACATGATCA CCGGTGCTGC CGAGATGGAC GCGCGATCC TGGTTTGCTC GGCTGCCGAC	60
GGCCCGATGC CACAGACCCG CGAGCACATC CTGCTTGCCC GTCAGGTGGG CGTTCCGGCC	120

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ATCGTCGTGT TCCTCAACAA GGTGACGACCAG GTTGACGACG CCGAGCTTCT CGAGCTCGTC 180
 GAGCTTGAAG TTCGCGAACT TCTGTGCTCC TACGACTTCC CGGGCGACGA TATCCCGATC 240
 ATCAAGGGTT CGGCACTTGC TGCTCTTGAA GATTCTGACA AGAAGATCGG TGAAGACGCG 300
 ATCCGCGAGC TGATGGCTGC TGTCGACGCC TACATCCCGA CGCCTGAGCG TCCGATCGAC 360
 CAGCCGTTCC TGATGCCGAT CGAAGACGTG TTCTCGATCT CGGGTCGTGG TACGGTTGTG 420
 ACGGGTCGCG TTGAGCGCGG TATCGTCAAG GTTGGTGAAG AAGTCGAAAT CGTCGGCATC 480
 CGTCCGACCT CGAAGACGAC TGTTACCGGC GTTGAAATGT TCCGCAAGCT GCTCGACCAG 540
 GGCCAGGCCG GCGACAACAT CCGTGCACTC GTTCGCGGCG TTACCCGTGA CGGCGTCGAG 600
 CGTGGTCAGA TCCTGTGCAA GCCGGGTTTCG GTCAAGCCGC ACAAGAAGTT CATGGCAGAA 660
 GCCTACATCC TGACGAAGGA AGAAGGCGGC CGTCATACGC CGTTCTTCAC GAACTACCGT 720
 CCGCAGTTCT ACTTCCGTAC GACTGACGTT ACCGGTATCG TTTCGCTTCC TGAAGGCACG 780
 GAAATGGTTA TGCCTGGCGA CAACGTCACT GTTGAAGTCG AGCTGATCGT TCCGATCGCG 840
 ATGGAAGAAA AGCTGCGCTT CGCTATCCGC GAAGGCGGCC GTACCGTCGG CGCCGGC 897

(2) INFORMATION FOR SEQ ID NO: 148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 885 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus subtilis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148:

ATGATCACTG GTGCTGCGCA AATGGACGGA GCTATCCTTG TAGTATCTGC TGCTGATGGC 60
 CCAATGCCAC AAACCTCGTGA GCACATCCTT CTTTCTAAAA ACGTTGGTGT ACCATACATC 120
 GTTGTATTCT TAAACAAATG CGACATGGTA GACGACGAAG AGCTTCTTGA ACTAGTTGAA 180
 ATGGAAGTTC GCGATCTTCT TAGCGAATAC GACTTCCCTG GTGATGATGT ACCAGTTGTT 240
 AAAGGTTCTG CTCTTAAAGC TCTTGAAGGA GACGCTGAGT GGGAAGCTAA AATCTTCGAA 300
 CTTATGGATG CGGTTGATGA GTACATCCCA ACTCCAGAAC GCGACACTGA AAAACCATTC 360
 ATGATGCCAG TTGAGGACGT ATTCTCAATC ACTGGTCGTG GTACAGTTGC TACTGGCCGT 420
 GTAGAACGCG GACAAGTTAA AGTCGGTGAC GAAGTTGAAA TCATCGGTCT TCAAGAAGAG 480

AACAAGAAAA CAACTGTTAC AGGTGTTGAA ATGTTCCGTA AGCTTCTTGA TTACGCTGAA 540
GCTGGTGACA ACATTGGTGC CCTTCTTCGC GGTGTATCTC GTGAAGAAAT CCAACGTGGT 600
CAAGTACTTG CTAAACCAGG TACAATCACT CCACACAGCA AATTCAAAGC TGAAGTTTAC 660
GTTCTTTCTA AAGAAGAGGG TGGACGTCAT ACTCCATTCT TCTCTAACTA CCGTCCTCAG 720
TTCTACTTCC GTACAACTGA CGTAACTGGT ATCATCCATC TTCCAGAAGG CGTAGAAATG 780
GTTATGCCTG GAGATAACAC TGAAATGAAC GTTGAACCTA TTTCTACAAT CGCTATCGAA 840
GAAGGAACTC GTTTCTCTAT TCGTGAAGGC GGACGTACTG TTGGT 885

(2) INFORMATION FOR SEQ ID NO: 149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 882 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacteroides fragilis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:

ATGGTTACTG GTGCTGCTCA GATGGACGGT GCTATCATTG TAGTTGCTGC TACTGATGGT 60
CCGATGCCTC AGACTCGTGA GCACATCCTT TTGGCTCGTC AGGTAAACGT TCCGAAGCTG 120
GTTGTATTCA TGAACAAGTG CGATATGGTT GAAGATGCTG AGATGTTGGA ACTTGTGAA 180
ATGGAAATGA GAGAATTGCT TTCATTCTAT GATTTCGACG GTGACAATAC TCCGATCATT 240
CAGGGTTCTG CTCTTGGTGC ATTGAACGGC GTAGAAAAAT GGGAAGACAA AGTAATGGAA 300
CTGATGGAAG CTGTTGATAC TTGGATTCCA CTGCCTCCGC GCGATGTTGA TAAACCTTTC 360
TTGATGCCGG TAGAAGACGT GTTCTCTATC ACAGGTCGTG GTACTGTAGC TACAGGTCGT 420
ATCGAAACTG GTGTTATCCA TGTAGGTGAT GAAATCGAAA TCCTCGGTTT GGGTGAAGAT 480
AAGAAATCAG TTGTAACAGG TGTGAAATG TTCCGCAAAC TTCTGGATCA GGGTGAAGCT 540
GGTGACAACG TAGGTCTGTT GCTTCGTGGT GTTGACAAGA ACGAAATCAA ACGTGGTATG 600
GTTCTTTGTA AACCAGGTCA GATTAAACCT CACTCTAAAT TCAAAGCAGA GGTTCATATC 660
CTGAAGAAAG AAGAAGGTGG TCGTCACACT CCATTCCATA ACAAATATCG TCCTCAGTTC 720
TACCTGCGTA CTATGGACTG TACAGGTGAA ATCACTCTTC CGGAAGGAAC TGAAATGGTA 780
ATGCCGGGTG ATAACGTAAC TATCACTGTA GAGTTGATCT ATCCGGTTGC ACTGAACATC 840

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GGTCTTCGTT TCGCTATCCG CGAAGGTGGA CGTACAGTAG GT

882

(2) INFORMATION FOR SEQ ID NO: 150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 888 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Borrelia burgdorferi*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 150:

AATATGATTA CAGGAGCAGC TCAAATGGAT GCAGCGATAC TTTTAGTTGC TGCTGATAGT	60
GGTGCTGAGC CTCAAACAAA AGAGCATTTG CTTCTTGCTC AAAGAATGGG AATAAAGAAA	120
ATAATAGTTT TTTTAAATAA ATTGGACTTA GCAGATCCTG AACTTGTTGA GCTTGTTGAA	180
GTTGAAGTTT TAGAACTTGT TGAAAAATAT GGCTTTTCAG CTGATACTCC AATAATCAAA	240
GGTTCAGCTT TTGGGGCTAT GTCAAATCCA GAAGATCCTG AATCTACAAA ATGCGTTAAA	300
GAAGTTCTTG AATCTATGGA TAATTATTTT GATCTTCCAG AAAGAGATAT TGACAAGCCA	360
TTTTTGCTTG CTGTTGAAGA TGTATTTTCT ATTTTCAGGAA GAGGCACTGT TGCTACTGGG	420
CGTATTGAAA GAGGTATTAT TAAAGTTGGT CAAGAAGTTG AAATAGTTGG AATTAAAGAA	480
ACCAGAAAAA CTAAGTTTAC TGGTGTGAA ATGTTCCAGA AAATTCTTGA GCAAGGTCAA	540
GCAGGGGATA ATGTTGGTCT TCTTTTGAGA GGC GTTGATA AAAAAGACAT TGAGAGGGGG	600
CAAGTTTGT CAGCTCCAGG TACAATTACT CCACACAAGA AATTTAAAGC TTCAATTTAT	660
TGTTTGACTA AAGAAGAAGG CGGTAGGCAC AAGCCATTTT TCCCAGGGTA TAGACCACAG	720
TTCTTTTTTA GAACAACCGA TGTTACTGGA GTTGTTGCTT TAGAGGGCAA AGAAATGGTT	780
ATGCCTGGTG ATAATGTTGA TATTATTGTT GAGCTGATCT CTTCAATAGC TATGGATAAG	840
AATGTAGAAT TTGCTGTTCT AGAAGGTGGA AGAACCGTTG CTT CAGGA	888

(2) INFORMATION FOR SEQ ID NO: 151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 894 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

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(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Brevibacterium linens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151:

AACATGATCA CCGGTGCCGC TCAGATGGAC GGTGCGATCC TCGTCGTCGC CGCTACCGAC 60
GGACCGATGC CCCAGACCCG TGAGCACGTG CTGCTCGCGC GTCAGGTCGG CGTTCCCTAC 120
ATCGTCGTGG CTCTGAACAA GTCCGACATG GTCGATGACG AGGAGCTCCT CGAGCTCGTC 180
GAATTCGAGG TCCGCGACCT GCTCTCGAGC CAGGACTTCG ACGGAGACAA CGCTCCGGTC 240
ATTCCGGTGT CCGCTCTCAA GGCCTGGAA GGCACGAGA AGTGGGTCAA GAGCGTTCAG 300
GATCTCATGG CTGCCGTCGA TGACAACGTT CCGGAGCCGG AGCGCGATGT CGACAAGCCG 360
TTCCTCATGC CCGTCGAGGA CGTCTTCACG ATCACC GGTC GTGGAACCGT CGTCACCGGT 420
CGTGTCGAGC GCGGCGTGCT CCTGCCTAAC GACGAAATCG AAATCGTCGG CATCAAGGAG 480
AAGTCGTCCA AGACGACTGT CACCGCTATC GAGATGTTCC GCAAGACCCT GCCGGATGCC 540
CGTGCAGGTG AGAACGTCGG TCTGCTCCTC CGCGGCACCA AGCGCGAGGA TGTTGAGCGC 600
GGTCAGGTCA TCGTGAAGCC GGGTTCGATC ACCCGCACCA CCAAGTTCGA GGCTCAGGTC 660
TACATCCTGA GCAAGGACGA GGGCGGACGT CACAACCCGT TCTACTCGAA CTACCGTCCG 720
CAGTTCTACT TCCGACCAC GGACGTCACC GGTGTCATCA CGCTGCCCCA GGGCACCGAG 780
ATGGTCATGC CCGGCGACAA CACCGATATG TCGGTCGAGC TCATCCAGCC GATCGCTATG 840
GAGGACCGCC TCCGCTTCGC AATCCGCGAA GGTGGCCGCA CCGTCGGCGC CGGT 894

(2) INFORMATION FOR SEQ ID NO: 152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 888 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Burkholderia cepacia*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152:

ATGATCACGG GCGCAGCGCA GATGGACGGC GCGATCCTGG TTTGCTCGGC AGCAGACGGC 60
CCGATGCCGC AAACGCGTGA GCACATCCTG CTGGCGCGTC AGGTTGGTGT TCCGTACATC 120
ATCGTGTTC TGAACAAGTG CGACAGTGTG GACGACGCTG AACTGCTCGA GCTGGTCGAG 180

ATGGAAGTTC GCGAACTCCT GTCGAAGTAC GACTTCCCGG GCGACGACAC GCCGATCGTG 240
AAGGGTTTCGG CCAAGCTGGC GCTGGAAGGC GACACGGGCG AGCTGGGCGA AGTGGCGATC 300
ATGAGCCTGG CAGACGCGCT GGACACGTAC ATCCCGACGC CGGAGCGTGC AGTTGACGGC 360
GCGTTCCTGA TGCCGGTGGA AGACGTGTTT TCGATCTCGG GCCGTGGTAC GGTGGTGACG 420
GGTCGTGTCTG AGCGCGGCAT CGTGAAGGTC GGC GAAGAAA TCGAAATCGT CGGTATCAAG 480
CCGACGGTGA AGACGACCTG CACGGGCGTT GAAATGTTCC GCAAGCTGCT GGACCAAGGT 540
CAGGCAGGCG ACAACGTCGG TATCCTGCTG CGCGGCACGA AGCGTGAAGA CGTGGAGCGT 600
GGCCAGGTTC TGGCGAAGCC GGGTTCGATC ACGCCGCACA CGCACTTCAC GGCTGAAGTG 660
TACGTGCTGA GCAAGGACGA AGGCGGCCGT CACACGCCGT TCTTCAACAA CTACCGTCCG 720
CAGTTCTACT TCCGTACGAC GGACGTGACG GGCTCGATCG AGCTGCCGAA GGACAAGGAA 780
ATGGTGATGC CGGGCGACAA CGTGTCGATC ACGGTGAAGC TGATTGCTCC GATCGCGATG 840
GAAGAAGGTC TGCGCTTCGC AATCCGTGAA GCGGCCGTA CGGTCGGC 888

(2) INFORMATION FOR SEQ ID NO: 153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 891 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Chlamydia trachomatis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:

AACATGATCA CCGGTGCGGC TCAAATGGAC GGGGCTATTC TAGTAGTTTC TGCAACAGAC 60
GGAGCTATGC CTCAAATAA AGAGCATATT CTTTGGCAA GACAAGTTGG GGTTCCTTAC 120
ATCGTTGTTT TTCTCAATAA AATTGACATG ATTTCCGAAG AAGACGCTGA ATTGGTCGAC 180
TTGGTTGAGA TGGAGTTGGC TGAGCTTCTT GAAGAGAAAAG GATACAAAGG GTGTCCAATC 240
ATCAGAGGTT CTGCTCTGAA AGCTTTGGAA GGAGATGCTG CATACATAGA GAAAGTTCGA 300
GAGCTAATGC AAGCCGTCGA TGATAATATC CCTACTCCAG AAAGAGAAAT TGACAAGCCT 360
TTCTTAATGC CTATTGAGGA CGTGTCTCTT ATCTCCGAC GAGGAACTGT AGTAACTGGA 420
CGTATTGAGC GTGGAATTGT TAAAGTTTCC GATAAAGTTC AGTTGGTCGG TCTTAGAGAT 480
ACTAAAGAAA CGATTGTTAC TGGGGTTGAA ATGTTTCAGAA AAGAACTCCC AGAAGGTCGT 540

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(2) INFORMATION FOR SEO ID NO: 154:

(A) LENGTH: 891 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEO ID NO: 154:

AACATGATCA	CCGGTGCTGC	GCAGATGGAC	GGCGCGATCC	TGGTAGTTGC	TGCGACTGAC	60
GGCCCCGATGC	CGCAGACTCG	TGAGCACATC	CTGCTGGGTC	GTCAGGTAGG	CGTTC CGTAC	120
ATCATCGTGT	TCCTGAACAA	ATGCGACATG	GTTGATGACG	AAGAGCTGCT	GGAAC TGGTT	180
GAAATGGAAG	TTCGTGAACT	TCTGTCTCAG	TACGACTTCC	CGGGCGACGA	CACTCCGATC	240
GTTCGTGGTT	CTGCTCTGAA	AGCGCTGGAA	GGCGACGCAG	AGTGGGAAGC	GAAAA TCCTG	300
GAACTGGCTG	GCTTCCTGGA	TTCTTACATT	CCGGAACCAG	AGCGTGCGAT	TGACAAGCCG	360
TTCCTGCTGC	CGATCGAAGA	CGTATTCTCC	ATCTCCGGTC	GTGGTACCGT	TGTTACCGGT	420
CGTGTAGAAC	GCGGTATCAT	CAAAGTTGGT	GAAGAAGTTG	AAATCGTTGG	TATCAAAGAG	480
ACTCAGAAGT	CTACCTGTAC	TGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	CGAAGGCCGT	540
GCTGGTGAGA	ACGTAGGTGT	TCTGCTGCGT	GGTATCAAAC	GTGAAGAAAT	CGAACGTGGT	600
CAGGTACTGG	CTAAGCCGGG	CACCATCAAG	CCGCACACCA	AGTTCGAATC	TGAAGTGTAC	660
ATTCTGTCCA	AAGATGAAGG	CGGCCGTCAT	ACTCCGTTCT	TCAAAGGCTA	CCGTCCGCAG	720
TTCTACTTCC	GTACTACTGA	CGTGA CTGGT	ACCATCGAAC	TGCCGGAAGG	CGTAGAGATG	780
GTAATGCCGG	GCGACAACAT	CAAAATGGTT	GTTACCCTGA	TCCACCCGAT	CGCGATGGAC	840
GACGGTCTGC	GTTTCGCAAT	CCGTGAAGGC	GGCCGTACCG	TTGGCGCGGG	C	891

(2) INFORMATION FOR SEQ ID NO: 155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 891 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Fibrobacter succinogenes*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155:

AACATGGTGA CTGGTGCTGC TCAGATGGAC GCGCTATCC TCGTTGTTGC CGCTACTGAC 60
GGTCCGATGC CGCAGACTCG CGAACACATC CTTCTCGCTC ACCAGGTTGG CGTGCCGAAG 120
ATCGTCGTGT TCATGAACAA GTGCGACATG GTTGACGATG CTGAAATTCT CGACCTCGTC 180
GAAATGGAAG TTCGCGAACT CCTCTCCAAG TATGACTTCG ACGGTGACAA CACCCCGATC 240
ATCCGTGGTT CCGCTCTCAA GGCCCTCGAA GCGGATCCGG AATACCAGGA CAAGGTCATG 300
GAACTCATGA ACGCTTGCGA CGAATACATC CCGCTCCCGC AGCGCGATAC CGACAAGCCG 360
TTCCTCATGC CGATCGAAGA CGTGTTACAG ATTACTGGCC GCGGCACTGT CGCTACTGGC 420
CGTATCGAAC GCGGTGTCGT TCGCTTGAAC GACAAGGTTG AACGTATCGG TCTCGGTGAA 480
ACCACCGAAT ACGTCATCAC CCGTGTGAA ATGTTCCGTA AGCTCCTCGA CGACGCTCAG 540
GCAGGTGACA ACGTTGGTCT CCTCCTCCGT GGTGCTGAAA AGAAGGACAT CGTCCGTGGC 600
ATGGTTCTCG CAGCTCCGAA GTCTGTCACT CCGCACACCG AATTTAAGGC TGAAATCTAC 660
GTTCTCACGA AGGACGAAGG TGGCCGTCAC ACGCCGTTCA TGAATGGCTA CCGTCCGCAG 720
TTCTACTTCC GCACCACCGA CGTTACTGGT ACGATCCAGC TCCCGGAAGG TGTCGAAATG 780
GTTACTCCGG GTGACACGGT CACGATCCAC GTGAACCTCA TCGCTCCGAT CGCTATGGAA 840
AAGCAGCTCC GCTTCGCTAT CCGTGAAGGT GGACGTACTG TTGGTGCTGG C 891

(2) INFORMATION FOR SEQ ID NO: 156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 894 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Flavobacterium ferrugineum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 156:

AACATGATCA CCGGTGCTGC CCAGATGGAC GGTGCTATCT TAGTTGTGGC TGCATCAGAC 60
GGTCCTATGC CTCAAACAAA AGAACACATC CTGCTTGCTG CCCAGGTAGG TGTACCTAAA 120
ATGGTTGTGT TTCTGAATAA AGTTGACCTC GTTGACGACG AAGAGCTCCT GGAGCTGGTT 180
GAGATCGAGG TTCGCGAAGA ACTGACTAAA CGCGGTTTCG ACGGCGACAA CACTCCAATC 240
ATCAAAGGTT CCGCTACAGG CGCCCTCGCT GGTGAAGAAA AGTGGGTAA AGAAATTGAA 300
AACCTGATGG ACGCTGTTGA CAGCTACATC CCACTGCCTC CTCGTCCGGT TGATCTGCCG 360
TTCCTGATGA GCGTAGAGGA CGTATTCTCT ATCACTGGTC GTGGTACTGT TGCTACCGGT 420
CGTATCGAGC GTGGCCGTAT CAAAGTTGGT GAGCCTGTTG AGATCGTAGG TCTGCAGGAG 480
TCTCCCCTGA ACTCTACCGT TACAGGTGTT GAGATGTTCC GCAAACCTCT CGACGAAGGT 540
GAAGCTGGTG ATAACGCCGG TCTCCTCCTC CGTGGTGTG AAAAAACACA GATCCGTCGC 600
GGTATGGTAA TCGTTAAACC CGGTTCCATC ACTCCGCACA CGGACTTCAA AGGCGAAGTT 660
TACGTACTGA GCAAAGACGA AGGTGGCCGT CACACTCCAT TCTTCAACAA ATACCGTCCT 720
CAATTCTACT TCCGTACAAC TGACGTTACA GGTGAAGTAG AACTGAACGC AGGAACAGAA 780
ATGGTTATGC CTGGTGATAA CACCAACCTG ACCGTTAAAC TGATCCAACC GATCGCTATG 840
GAAAAAGGTC TGAAATTCGC GATCCGCGAA GGTGGCCGTA CCGTAGGTGC AGGA 894

(2) INFORMATION FOR SEQ ID NO: 157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 891 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Haemophilus influenzae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157:

AATATGATTA CTGGTGCGGC ACAAATGGAT GGTGCTATTT TAGTAGTAGC AGCAACAGAT 60
GGTCCTATGC CACAACTCG TGAACACATC TTATTAGGTC GCCAAGTAGG TGTTCCATAC 120
ATCATCGTAT TCTTAAACAA ATGCGACATG GTAGATGACG AAGAGTTATT AGAATTAGTC 180
GAAATGGAAG TTCGTGAACT TCTATCTCAA TATGACTTCC CAGGTGACGA TACACCAATC 240

(2) INFORMATION FOR SEO ID NO: 158:

(A) LENGTH: 906 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158:

AACATGATCA	CCGGTGCGGC	GCAAAATGGAC	GGAGCGATTT	TGGTTGTTTC	TGCAGCTGAT	60
GGCCCTATGC	CTCAAAC TAG	GGAGCATATC	TTATTGTCTC	GTCAAGTAGG	CGTGCCTCAC	120
ATCGTTGTTT	TCTTAAACAA	ACAAGACATG	G TAGATGACC	AAGAATTGTT	AGAACTTGTA	180
GAAATGGAAG	TGCGCGAATT	GTTGAGCGCG	TATGAATTTT	CTGGCGATGA	CACTCCTATC	240
G TAGCGGGTT	CAGCTTTAAG	AGCTTTAGAA	GAAGCAAAGG	CTGGTAATGT	GGGTGAATGG	300
GGTGAAAAAG	TGCTTAAACT	TATGGCTGAA	GTGGATGCCT	ATATCCCTAC	TCCAGAAAAG	360
GACACTGAAA	AAACTTTCTT	GATGCCGGTT	GAAGATGTGT	TCTCTATTGC	GGGTAGAGGG	420
ACTGTGGTTA	CAGGTAGGAT	TGAAAGAGGC	GTGGTGAAAG	TAGGCGATGA	AGTGGAATC	480
GTTGGTATCA	GACCTACACA	AAAAACGACT	GTAACCGGTG	TAGAAATGTT	TAGGAAAGAG	540
TTGGAAAAAG	GTGAAGCCGG	CGATAATGTG	GGCGTGCTTT	TGAGAGGAAC	TAAAAAGAA	600

GAAGTGGAAC GCGGTATGGT TCTATGCAAA CCAGGTTCTA TCACTCCGCA CAAGAAATTT 660
GAGGGAGAAA TTTATGTCCT TTCTAAAGAA GAAGGCGGGA GACACACTCC ATTCTTCACC 720
AATTACCGCC CGCAATTCTA TGTGCGCACA ACTGATGTGA CTGGCTCTAT CACCCTTCCT 780
GAAGGCGTAG AAATGGTTAT GCCTGGCGAT AATGTGAAAA TCACTGTAGA GTTGATTAGC 840
CCTGTTGCGT TAGAGTTGGG AACTAAATTT GCGATTCGTG AAGGCGGTAG GACCGTTGGT 900
GCTGGT 906

(2) INFORMATION FOR SEQ ID NO: 159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 891 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Micrococcus luteus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159:

AACATGATCA CCGGCGCCGC TCAGATGGAC GCGCGATCC TCGTGGTCGC CGCTACCGAC 60
GGCCCGATGG CCCAGACCCG TGAGCACGTG CTCCTGGCCC GCCAGGTCGG CGTGCCGGCC 120
CTGCTCGTGG CCCTGAACAA GTCGGACATG GTGGAGGACG AGGAGCTCCT CGAGCGTGTC 180
GAGATGGAGG TCCGGCAGCT GCTGTCCTCC AGGAGCTTCG ACGTCGACGA GGCCCCGGTC 240
ATCCGCACCT CCGCTCTGAA GGCCCTCGAG GCGGACCCCC AGTGGGTCAA GTCCGTCGAG 300
GACCTCATGG ATGCCGTGGA CGAGTACATC CCGGACCCGG TCGCGACAA GGACAAGCCG 360
TTCCTGATGC CGATCGAGGA CGTCTTCACG ATCACC GGCC GTGGCACC GTGACCGGT 420
CGCGCCGAGC GCGGCACCCT GAAGATCAAC TCCGAGGTCG AGATCGTCGG CATCCGCGAC 480
GTGCAGAAGA CCACTGTCAC CGGCATCGAG ATGTTCCACA AGCAGCTCGA CGAGGCCTGG 540
GCCGGCGAGA ACTGCGGTCT GCTCGTGCGC GGTCTGAAGC GCGACGACGT CGAGCGCGGC 600
CAGGTGCTGG TGGAGCCGGG CTCCATCACC CCGCACACCA ACTTCGAGGC GAACGTCTAC 660
ATCCTGTCCA AGGACGAGGG TGGGCGTCAC ACCCCGTTCT ACTCGAACTA CCGCGCGCAG 720
TTCTACTTCC GCACCACCGA CGTCACCGGC GTCATCACGC TGCCCCGAGGG CACCGAGATG 780
GTCATGCCCC GCGACACCAC CGAGATGTCG GTCGAGCTCA TCCAGCCGAT CGCCATGGAG 840
GAGGGCCTCG GCTTCGCCAT CCGCGAGGGT GGCCGCACCG TGGGCTCCGG C 891

0909643-12001

(2) INFORMATION FOR SEQ ID NO: 160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 891 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 160:

AACATGATCA CCGGCGCCGC GCAGATGGAC GGTGCGATCC TGGTGGTCGC CGCCACCGAC 60
GGCCCGATGC CCCAGACCCG CGAGCACGTT CTGCTGGCGC GTCAAGTGGG TGTGCCCTAC 120
ATCCTGGTAG CGCTGAACAA GGCCGACGCA GTGGACGACG AGGAGCTGCT CGAACTCGTC 180
GAGATGGAGG TCCGCGAGCT GCTGGCTGCC CAGGAATTCG ACGAGGACGC CCCGGTTGTG 240
CGGGTCTCGG CGCTCAAGGC GCTCGAGGGT GACGCGAAGT GGGTTGCCTC TGTCGAGGAA 300
CTGATGAACG CGGTGACGA GTCGATTCCG GACCCGGTCC GCGAGACCGA CAAGCCGTTC 360
CTGATGCCGG TCGAGGACGT CTTCAACATT ACCGGCCGCG GAACCGTGGT CACCGGACGT 420
GTGGAGCGCG GCGTGATCAA CGTGAACGAG GAAGTTGAGA TCGTCGGCAT TCGCCCATCG 480
ACCACCAAGA CCACCGTCAC CGGTGTGGAG ATGTTCCGCA AGCTGCTCGA CCAGGGCCAG 540
GCGGGCGACA ACGTTGGTTT GCTGCTGCGG GCGTCAAGC GCGAGGACGT CGAGCGTGGC 600
CAGGTTGTCA CCAAGCCCGG CACCACCACG CCGCACACCG AGTTCGAAGG CCAGGTCTAC 660
ATCCTGTCCA AGGACGAGGG CGGCCGGCAC ACGCCGTTCT TCAACAATA CCGTCCGCAG 720
TTCTACTTCC GCACCACCGA CGTGACCGGT GTGGTGACAC TGCCGGAGGG CACCGAGATG 780
GTGATGCCCG GTGACAACAC CAACATCTCG GTGAAGTTGA TCCAGCCCGT CGCCATGGAC 840
GAAGGTCTGC GTTTCGCGAT CCGCGAGGGT GGCCGCACCG TGGGCGCCGG C 891

(2) INFORMATION FOR SEQ ID NO: 161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 891 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycoplasma genitalium*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161:

AATATGATCA CAGGTGCTGC ACAAATGGAT GGAGCTATTC TAGTTGTTTC AGCAACTGAT	60
AGTGTGATGC CCCAAACCCG CGAGCACATC TTAAGTGGCC GCCAAGTAGG GGTTCCTAAA	120
ATGGTAGTTT TTCTAAACAA GTGTGATATT GCTAGTGATG AAGAGGTACA AGAACTTGTT	180
GCTGAAGAAG TACGTGATCT GTTAACCTCC TATGGTTTTG ATGGTAAGAA CACTCCTATT	240
ATTTATGGCT CAGCTTTAAA AGCATTGGAA GGTGATCCAA AGTGGGAGGC TAAGATCCAT	300
GATTTGATTA AAGCAGTTGA TGAATGGATT CCAACTCCTA CACGTGAAGT AGATAAACCT	360
TTCTTATTAG CAATTGAAGA TACGATGACC ATTACTGGTA GAGGTACAGT TGTTACAGGA	420
AGAGTTGAAA GAGGTGAACT CAAAGTAGGT CAAGAAGTTG AAATTGTTGG TTAAAAACCA	480
ATTAGAAAAG CAGTTGTTAC TGGAATTGAA ATGTTCAAAA AGGAACTTGA TTCAGCAATG	540
GCTGGTGACA ATGCTGGGGT ATTATTACGT GGTGTTGAAC GTAAAGAAGT TGAAAGAGGT	600
CAAGTTTTAG CAAAACCAGG CTCTATTAAA CCGCACAAGA AATTTAAAGC TGAGATCTAT	660
GCTTTAAAGA AAGAAGAAGG TGGTAGACAC ACTGGTTTTT TAAACGGTTA CCGTCCTCAA	720
TTCTATTTCC GTACCACTGA TGTAACGGT TCTATTGCTT TAGCTGAAAA TACTGAAATG	780
GTTCTACCTG GTGATAATGC TTCTATTACT GTTGAGTTAA TTGCTCCTAT CGCTTGTGAA	840
AAAGGTAGTA AGTTCTCAAT TCGTGAAGGT GGTAGAACTG TAGGGGCAGG C	891

(2) INFORMATION FOR SEQ ID NO: 162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 891 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Neisseria gonorrhoeae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 162:

AACATGATTA CCGGCGCCGC ACAAATGGAC GGTGCAATCC TGGTATGTTT TGCTGCCGAC	60
GGCCCTATGC CGCAAACCCG CGAACACATC CTGCTGGCCC GTCAAGTAGG CGTACCTTAC	120
ATCATCGTGT TCATGAACAA ATGCGACATG GTCGACGATG CCGAGCTGTT CCAACTGGTT	180
GAAATGGAAT TCCGCGACCT GCTGTCCAGC TACGACTTCC CCGGCGACGA CTGCCCGATC	240

GTACAAGGTT CCGCACTGAA AGCCTTGGA GGCATGCCG CTTACGAAGA AAAAATCTTC 300
GAACTGGCTA CCGCATTGGA CAGATACATC CCGACTCCCG AGCGTGCCGT GGACAAACCA 360
TTCCTGCTGC CTATCGAAGA CGTGTTCTCC ATTTCCGGCC GCGGTACCGT AGTCACCGGC 420
CGTGTAGAGC GAGGTATCAT CCACGTTGGT GACGAGATTG AAATCGTCGG TCTGAAAGAA 480
ACCCAAAAAA CCACCTGTAC CGGCGTTGAA ATGTTCCGCA AACTGCTGGA CGAAGGTCAG 540
GCGGGCGACA ACGTAGGCGT ATTGCTGCGC GGTACCAAAC GTGAAGACGT AGAACGCGGT 600
CAGGTATTGG CCAAACGGGG TACTATCACT CCTCACACCA AGTTCAAAGC AGAAGTGTAC 660
GTATTGAGCA AAGAAGAGGG CGGCCCCCAT ACCCCGTTTT TCGCCAACTA CCGTCCCCAA 720
TTCTACTTCC GTACCACTGA CGTAACCGGC ACGATTACTT TGGAAAAAGG TGTGGAAATG 780
GTAATGCCGG GTGAGAACGT AACCATTACT GTAGAACTGA TTGCGCCTAT CGCTATGGAA 840
GAAGGTCTGC GCTTTGCGAT TCGCGAAGGC GGCCGTACCG TGGGTGCCGG C 891

(2) INFORMATION FOR SEQ ID NO: 163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 891 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Rickettsia prowazekii*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163:

AATATGATAA CTGGTGCCGC TCAGATGGAT GGTGCTATAT TAGTAGTTTC TGCTGCTGAT 60
GGTCCTATGC CTCAAACCTAG AGAACATATA TTACTGGCAA AACAGGTAGG TGTACCTGCT 120
ATGGTAGTAT TTTTGAATAA AGTAGATATG GTAGATGATC CTGACCTATT AGAATTAGTT 180
GAGATGGAAG TAAGAGAATT ATTATCAAAA TATGGTTTCC CTGGTAATGA AATACCTATT 240
ATTAAAGGTT CTGCACTTCA AGCTTTAGAA GGAAAACCTG AAGGTGAAAA AGCTATTAAT 300
GAGTTAATGA ATGCAGTAGA TACGTATATA CCTCAGCCTA TAGAGCTACA AGATAAACCT 360
TTTTTAATGC CAATAGAGGA TGTATTTTCT ATTTCAGGCA GAGGTACCGT TGTAACCTGGT 420
AGAGTGGAGT CAGGCATAAT TAAGGTGGGT GAAGAAATTG AAATAGTAGG TCTAAAAAAT 480
ACGCAAAAAA CGACTTGTAC AGGTGTAGAA ATGTTTCAGAA AATTACTTGA TGAAGGACAA 540
TCTGGAGATA ATGTCGGTAT ATTACTACGT GGTACAAAAA GAGAAGAAGT AGAAAGAGGA 600

(2) INFORMATION FOR SEQ ID NO: 164:

(A) LENGTH: 891 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 164:

(2) INFORMATION FOR SEQ ID NO: 165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 881 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Shewanella putida*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165:

ATGATCACTG GTGCTGCACA GATGGACGGC GCGATTCTGG TAGTCGCTTC AACAGACGGT 60
CCAATGCCAC AGACTCGTGA GCACATCCTG CTTTCTCGTC AGGTTGGCGT ACCATTCATC 120
ATCGTATTCA TGAACAAATG TGACATGGTA GATGACGAAG AGCTGTTAGA GCTAGTTGAG 180
ATGGAAGTGC GTGAACTGTT ATCAGAATAC GATTTCCCAG GTGATGACTT ACCGGTAATC 240
CAAGGTTTCA CTCTGAAAGC GCTAGAAGGC GAGCCAGAGT GGGAAGCAAA AATCCTTGAA 300
TTAGCAGCGG CGCTGGATTC TTACATTCCA GAACCACAAC GTGACATCGA TAAGCCGTTC 360
CTACTGCCAA TCGAAGACGT ATTCTCAATT TCAGGCCGTG GTACAGTAGT AACAGGTCGT 420
GTTGAGCGTG GTATTGTACG CGTAGGCGAC GAAGTTGAAA TCGTTGGTGT ACGTGCGACA 480
ACTAAGACAA CGTGTACTGG TGTAGAAATG TTCCGTAAAC TGCTTGACGA AGGTCGTGCA 540
GGTGAGAACT GTGGTATTTT GTTACGTGGT ACTAAGCGTG ATGACGTAGA ACGTGGTCAA 600
GTATTAGCGA AGCCAGGTTT AATCAACCCA CACACTACTT TTGAATCAGA AGTTTACGTA 660
CTGTCAAAAG AAGAAGGTGG TCGTCACACG CCATTCTTCA AAGGCTACCG TCCACAGTTC 720
TACTTCCGTA CAACTGACGT AACC GG TACT ATCGAACTGC CAGAAGGCGT AGAGATGGTA 780
ATGCCAGGCG ATAACATCAA GATGGTAGTG ACACTGATTT GCCCAATCGC GATGGACGAA 840
GGTTTACGCT TCGCAATCCG TGAAGGCGGT CGTACAGTGG T 881

(2) INFORMATION FOR SEQ ID NO: 166:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 897 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Stigmatella aurantiaca*

09989643 12001

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 166:

AACATGATCA CGGGCGCGGC GCAGATGGAC GGAGCGATTC TGGTGGTGTC CGCGGCCGAC	60
GGCCCGATGC CCCAGACGCG TGAGCACATC CTGCTGGCCA GGCAGGTGGG CGTGCCCTAC	120
ATCGTCGTCT TCCTGAACAA GGTGGACATG CTGGACGATC CGGAGCTGCG CGAGCTGGTG	180
GAGATGGAGG TGCGCGACCT GCTCAAGAAG TACGAGTTCC CGGGCGACAG CATCCCCATC	240
ATCCCTGGCA GCGCGCTCAA GGCGCTGGAG GGAGACACCA GCGACATCGG CGAGGGAGCG	300
ATCCTGAAGC TGATGGCGGC GGTGGACGAG TACATCCCGA CGCCGACGCG TGCGACGGAC	360
AAGCCGTTCC TGATGCCGGT GGAAGACGTG TTCTCCATCG CAGGCCGAGG AACGGTGGCG	420
ACGGGCCGAG TGGAGCGCG CAAGATCAAG GTGGGCGAGG AAGTGGAGAT CGTGGGGATC	480
CGTCCGACGC AGAAGACGGT CATCACGGGG GTGGAGATGT TCCGCAAGCT GCTGGACGAG	540
GGCATGGCGG GAGACAACAT CGGAGCGCTG CTGCGAGGCC TGAAGCGCGA GGACCTGGAG	600
CGTGGGCAGG TGCTGGCGAA CTGGGGGAGC ATCAACCCGC ACACGAAGTT CAAGGCGCAG	660
GTGTACGTGC TGTCGAAGGA AGAGGGAGGG CGGCACACGC CGTTCTTCAA GGGATACCGG	720
CCGCAGTTCT ACTTCCGGAC GACGGACGTG ACCGGAACGG TGAAGCTGCC GGACAACGTG	780
GAGATGGTGA TGCCGGGAGA CAACATCGCC ATCGAGGTGG AGCTCATTAC TCCGGTCGCC	840
ATGGAGAAGG AGCTGCCGTT CGCCATCCGT GAGGGTGGCC GCACGGTGGG CGCCGGC	897

(2) INFORMATION FOR SEQ ID NO: 167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 894 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pyogenes*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167:

AACATGATCA CTGGTGCCGC TCAAATGGAC GGAGCTATCC TTGTAGTTGC TTCAACTGAT	60
GGACCAATGC CACAACTCG TGAGCACATC CTTCTTTCAC GTCAGGTTGG TGTAAACAC	120
CTTATCGTGT TCATGAACAA AGTTGACCTT GTTGATGACG AAGAGTTGCT TGAATTAGTT	180
GAGATGGAAA TTCGTGACCT TCTTTCAGAA TACGATTTC CAGGTGATGA CCTTCCAGTT	240
ATCCAAGGTT CAGCTCTTAA AGCTCTTGAA GGCGACACTA AATTTGAAGA CATCATCATG	300

GAATTGATGG ATACTGTTGA TTCATACATT CCAGAACCAG AACGCGACAC TGACAAACCA 360
TTGCTTCTTC CAGTCGAAGA CGTATTCTCA ATTACAGGTC GTGGTACAGT TGCTTCAGGA 420
CGTATCGACC GTGGTACTGT TCGTGTCAAC GACGAAATCG AAATCGTTGG TATCAAAGAA 480
GAAACTAAAA AAGCTGTTGT TACTGGTGTT GAAATGTTCC GTAAACAACT TGACGAAGGT 540
CTTGCAGGAG ACAACGTAGG TATCCTTCTT CGTGGTGTTT AACGTGACGA AATCGAACGT 600
GGTCAAGTTA TTGCTAAACC AAGTTCAATC AACCCACACA CTAAATTCAA AGGTGAAGTA 660
TATATCCTTT CTAAAGACGA AGGTGGACGT CACACTCCAT TCTTCAACAA CTACCGTCCA 720
CAATTCTACT TCCGTACAAC TGACGTAACA GGTTCATCG AACTTCCAGC AGGTACAGAA 780
ATGGTTATGC CTGGTGATAA CGTGACAATC AACGTTGAGT TGATCCACCC AATCGCCGTA 840
GAACAAGGTA CTACTTTCTC AATCCGTGAA GGTGGACGTA CTGTTGGTTC AGGT 894

(2) INFORMATION FOR SEQ ID NO: 168:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 897 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Thiobacillus cuprinus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168:

AACATGATCA CCGGTGCGGC CCAGATGGAC GGCGCCATCC TGGTCGTGTC CGCCGCCGAC 60
GGCCCCATGC CCCAAACCCG CGAGCACATC CTGCTGGCGC GTCAGGTGGG CGTGCCCTAC 120
ATCATCGTGT TCCTCAACAA GTGCGACATG GTCGACGACG CCGAGCTGCT CGAACTCGTC 180
GAGATGGAAG TGCGCGAGCT GCTGTCCAAG TACGACTTCC CCGGTGACGA CACCCCCATC 240
ATCAAGGGCT CGGCCAAGCT GGCCCTCGAA GGCACAAAGG GCGAACTGGG CGAAGGCGCC 300
ATTCTCAAGC TGGCCGAGGC CCTGGACACC TACATCCCCA CGCCCGAGCG GGCCGTCGAC 360
GGCGCGTTCC TCATGCCCGT GGAAGACGTG TTCTCCATCT CCGGGCGCGG CACGGTGGTC 420
ACCGGGCGTG TGGAGCGCGG CATCATCAAG GTCGGCGAGG AAATCGAGAT TGTCGGCCTC 480
AAGCCCACCC TCAAGACCAC CTGCACCGGC GTGGAAATGT TCAGGAAGCT GCTCGACCAG 540
GGCCAGGCCG GCGACAACGT CGGCATCTTG CTGCGCGGCA CCAAGCGCGA GGAAGTCGAG 600
CGCGGCCAGG TGCTGTGCAA ACCCGGCTCG ATCAAGCCCC ACACCCACTT CACCGCCGAG 660

09989613-12001

GTGTACGTGC TGAGCAAGGA CGAGGGCGGC CGCCACACCC CCTTCTTCAA CAACTACCGC 720
CCGCAGTTCT ACTTCCGCAC CACCGACGTC ACCGGCGCCA TCGAACTGCC CAAGGACAAG 780
GAAATGGTCA TGCCCGGCGA TAATGTGAGC ATCACCGTCA AGCTCATCGC CCCCATCGCC 840
ATGGAAGAAG GCCTGCGCTT CGCCATCCGC GAAGGCGGCC GCACCGTCGG CGCCGGC 897

(2) INFORMATION FOR SEQ ID NO: 169:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 894 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Treponema pallidum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169:

AATATGATCA CGGGTGCTGC GCAGATGGAC GGTGGTATTC TCGTCGTGTC TGCGCCTGAC 60
GGCGTTATGC CACAGACGAA GGAGCATCTT CTGCTCGCCC GTCAGGTTGG TGTTCCCTCC 120
ATCATTGTTT TTTTGAACAA GGTGATTTG GTTGATGATC CTGAGTTGCT AGAGCTGGTG 180
GAAGAAGAGG TCGGTGATGC GCTTGCTGGA TATGGGTTTT CGCGTGAGAC GCCTATCGTC 240
AAGGGGTCTG CGTTTAAAGC TCTGCAGGAT GGCGCTTCCC CGGAGGATGC AGCTTGATTT 300
GAGGAACTGC TTGCGGCCAT GGATTCCTAC TTTGAAGACC CAGTGCCTGA CGACGCAAGA 360
CCTTTCTTGC TCTCTATCGA GGATGTGTAC ACTATTTCTG GGCGTGGTAC CGTTGTCACG 420
GGGCGCATCG AATGTGGGGT AATTAGTCTG AATGAAGAGG TCGAGATCGT CGGGATTAAG 480
CCCACTAAGA AAACAGTGGT TACTGGCATT GAGATGTTTA ATAAGTTGCT TGATCAGGGA 540
ATTGCAGGTG ATAACGTGGG GCTGCTTTTG CGCGGGGTGG ATAAAAAGA GGTGAGCGC 600
GGTCAGGTGC TTTCTAAGCC CGGTTCTATT AAGCCACACA CCAAGTTTGA GGCGCAGATC 660
TACGTGCTCT CTAAGGAAGA GGGTGCCGT CACAGTCCTT TTTTCAAGG TTATCGTCCG 720
CAGTTTTTATT TTAGAACTAC TGACATTACC GGTACGATTT CTCTTCCTGA AGGGGTAGAC 780
ATGGTGAAGC CGGGGGATAA CACCAAGATT ATAGGTGAGC TCATCCACCC GATAGCTATG 840
GACAAGGGTC TGAAGCTTGC GATTCGTGAA GGGGGGCGCA CTATTGCTTC TGGT 894

(2) INFORMATION FOR SEQ ID NO: 170:

(i) SEQUENCE CHARACTERISTICS:

09985643 112001

- (A) LENGTH: 891 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Ureaplasma urealyticum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170:

AATATGATTA CAGGGGCAGC ACAAATGGAT GGAGCAATTT TAGTTATTGC TGCATCTGAT 60
GGGGTTATGG CTCAAATAA AGAACATATT TTATTAGCAC GTCAAGTTGG TGTTCACAAA 120
ATCGTTGTTT TCTTAAACAA ATGTGATTTT ATGACAGATC CAGATATGCA AGATCTTGTT 180
GAAATGGAAG TTCGTGAATT ATTATCTAAA TATGGATTTG ATGGCGATAA CACACCAGTT 240
ATTCGTGGTT CAGGTCTTAA GGCTTTAGAA GGAGATCCAG TTTGAGAAGC AAAAATTGAT 300
GAATTAATGG ACGCAGTTGA TTCATGAATT CCATTACCAG AACGTAGTAC TGACAAACCA 360
TTCTTATTAG CAATTGAAGA TGTATTCACA ATTTCAGGAC GTGGTACAGT AGTAACTGGA 420
CGTGTTGAAC GTGGTGTATT AAAAGTTAAT GATGAGGTTG AAATTGTTGG TCTAAAAGAC 480
ACTCAAAAAA CTGTTGTTAC AGGAATTGAA ATGTTTAGAA AATCATTAGA TCAAGCTGAA 540
GCTGGTGATA ATGCTGGTAT TTTATTACGT GGTATTAAAA AAGAAGATGT TGAACGTGGT 600
CAAGTACTTG TAAAACCAGG ATCAATTAAA CCTCACCGTA CTTTTACTGC TAAAGTTTAT 660
ATTCTTAAAA AAGAAGAAGG TGGACGTCAT ACACCTATTG TTTCAGGATA CCGTCCACAA 720
TTCTATTTTA GAACAACAGA TGTAACAGGT GCTATTTTAT TACCTGCTGG TGTGATTGTT 780
GTTATGCCAG GTGATGACGT TGAAATGACT GTAGAATTAA TTGCTCCAGT TGCGATTGAA 840
GATGGATCTA AATTCTCAAT CCGTGAAGGT GGTAAAACCTG TAGGTCATGG T 891

(2) INFORMATION FOR SEQ ID NO: 171:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 909 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Wolinella succinogenes*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:

AACATGATTA CAGGTGCTGC TCAAATGGAT GGC GCGATT C TTGTTGTTTC TCGGCGGAT 60
GGCCCCATGC CCCAAACTAG GGAGCACATT CTTCTTTCTC GACAAGTAGG CGTTCCTTAC 120
ATCGTGGTTT TCTTGAACAA AGAAGATATG GTTGATGACG CTGAGCTTCT TGAGCTTGTT 180
GAAATGGAAG TTAGAGAACT TCTTAGCAAC TACGACTTCC CTGGAGATGA CACTCCTATC 240
GTTGCAGGTT CCGCTCTTAA AGCTCTTGAA GAGGCTAACG ACCAGGAAAA TGTTGGCGAG 300
TGGGGCGAGA AAGTATTGAA GCTTATGGCT GAGGTTGACC GATATATTCC TACGCCTGAG 360
CGAGATGTGG ATAAGCCTTT CTTATGCCT GTTGAAGACG TATTCTCCAT CGCGGGTCGT 420
GGAACCGTTG TGACAGGAAG AATTGAAAGA GCGTGTTA AAGTCGGTGA CGAAGTAGAA 480
ATCGTTGGTA TCCGAAACAC ACAAAAAACA ACCGTAACG GCGTTGAGAT GTTCCGAAAA 540
GAGCTCGACA AGGGTGAGGC GGGTGACAAC GTTGGTGTTT TTTTGAGAGG CACCAAGAAA 600
GAAGATGTTG AGAGAGGTAT GGTCTTTGT AAAATAGGTT CTATCACTCC TCACACTAAC 660
TTTGAAGGTG AAGTTTACGT TCTTTCCAAA GAGGAAGGCG GACGACACAC TCCATTCTTC 720
AATGGATACC GACCTCAGTT CTATGTTAGA ACTACAGACG TTACCGGTTT TATCTCTCTT 780
CCTGAGGGCG TAGAGATGGT TATGCCTGGT GACAACGTTA AGATCAATGT TGAGCTTATC 840
GCTCCTGTAG CCCTCGAAGA GGGAACACGA TTCGCGATCC GTGAAGGTGG TCGAACCGTT 900
GGTGCGGGT 909

(2) INFORMATION FOR SEQ ID NO: 172:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION:6
 - (D) OTHER INFORMATION:/note= "n = inosine"

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION:12
 - (D) OTHER INFORMATION:/note= "n = inosine"

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION:18
 - (D) OTHER INFORMATION:/note= "n = inosine"

00999643 "172001"

TARTCNGTRA ANGCYTCNAC RCACAT

(2) INFORMATION FOR SEQ ID NO: 173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173:

TCTTTAGCAG AACAGGATGA A

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(2) INFORMATION FOR SEQ ID NO: 174:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 174:

GAATAATTCC ATATCCTCCG

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